

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 15:52:50 ; Search time 1784.1 Seconds  
(without alignments)  
8323.656 Million cell updates/sec

Title: US-09-759-112a-5

Perfect score: 363

Sequence: 1 caggttactctgaagagtc.....cctcagtcacgcgtctctca 363

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_cm.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_or.\*

21: em\_ov.\*

22: em\_pat.\*

23: em\_ph.\*

24: em\_pl.\*

25: em\_ro.\*

26: em\_sts.\*

27: em\_un.\*

28: em\_vi.\*

29: em\_htg\_hum.\*

30: em\_htg\_inv.\*

31: em\_htg\_other.\*

32: em\_htg\_mus.\*

33: em\_htg\_pln.\*

34: em\_htg\_rod.\*

35: em\_htg\_mam.\*

36: em\_htg\_vrt.\*

37: em\_sy.\*

38: em\_htgo\_hum.\*

39: em\_htgo\_mus.\*

40: em\_htgo\_other.\*

41: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	316.6	87.2	360	10	MMHCV3	X75097 M.musculus
2	314.6	86.7	420	10	AY090903	AY090903 Mus muscu
3	311.8	85.9	426	6	AX458152	AX458152 Sequence
4	305.4	84.1	360	10	MMU22977	U22977 Mus muscu
5	305.4	84.1	360	10	MMU22979	U22979 Mus muscu
6	305.4	84.1	360	10	MMU22994	U22994 Mus muscu
7	303.8	83.7	360	10	MMU22992	U22992 Mus muscu
8	303.6	83.6	366	6	E07584	E07584 Gene fragme
9	300.6	82.8	360	10	MMU22981	U22981 Mus muscu
10	300.6	82.8	360	10	MMU23010	U23010 Mus muscu
11	300.6	82.8	360	10	MMU23013	U23013 Mus muscu
12	300.6	82.8	361	10	MMU23004	U23004 Mus muscu
13	299.6	82.5	360	10	MMU22999	U22999 Mus muscu
14	299.2	82.4	738	6	E07990	E07990 DNA encodin
15	298.6	82.3	358	10	I45910	I45910 Sequence 6
16	298.6	82.3	358	10	MMU23002	U23002 Mus muscu
17	295.8	81.5	360	10	MMU22983	U22983 Mus muscu
18	295.8	81.5	360	10	MMU22984	U22984 Mus muscu
19	295.8	81.5	360	10	MMU23005	U23005 Mus muscu
20	295.8	81.5	360	10	MMU23009	U23009 Mus muscu
21	294.4	81.1	360	10	MMU22997	U22997 Mus muscu
22	294.2	81.0	366	10	MMUGMSMJ	X53097 Mouse mRNA
23	293.8	80.9	358	10	MMU23000	U23000 Mus muscu
24	293.4	80.8	359	10	MMU23007	U23007 Mus muscu
25	293.2	80.8	438	10	S75897	S75897 Ig VH-19g h
26	291.4	80.3	365	10	MMU22929	U22929 Mus muscu
27	291	80.2	418	6	AR026944	AR026944 Sequence
28	290.4	80.0	348	10	MMHCV3	X75098 M.musculus
29	289.8	79.8	365	10	MMU22905	U22905 Mus muscu
30	289.8	79.8	365	10	MMU22909	U22909 Mus muscu
31	289.8	79.8	365	10	MMU22911	U22911 Mus muscu
32	289.8	79.8	365	10	MMU22926	U22926 Mus muscu
33	289.8	79.8	365	10	MMU22956	U22956 Mus muscu
34	289.8	79.8	365	10	MMU22957	U22957 Mus muscu
35	289.8	79.8	195281	10	AC073939	AC073939 Mus muscu
36	289.6	79.8	360	10	MMU22988	U22988 Mus muscu
37	289.2	79.7	326	10	MMU22986	U22986 Mus muscu
38	288.4	79.4	363	10	S62427	S62427 anti-paragu
39	288.2	79.4	365	10	MMU22955	U22955 Mus muscu
40	287.8	79.3	1410	10	MMU421677	MMU421677 Mus muscu
41	285.6	78.7	357	10	S63186	S63186 Ig VH-anti-
42	285	78.5	318	10	MMU22990	U22990 Mus muscu
43	285	78.5	330	10	MMU22975	U22975 Mus muscu
44	282.8	77.9	353	10	MMU22995	U22995 Mus muscu
45	281.8	77.6	365	10	MMU22907	U22907 Mus muscu

#### ALIGNMENTS

RESULT 1	MMHCV3	MMHCV3	360 bp	mRNA	linear	ROD 23-FEB-1994
LOCUS	M.musculus	(A.SW)	mRNA for ASWB1 antibody heavy chain variable			
DEFINITION	region.					
ACCESSION	X75097					
VERSION	X75097.1	GI:414165				
KEYWORDS	antibody; variable region; VH region.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	1 (bases 1 to 360)					
AUTHORS	Monastier M., Lozman M.J., Novick K.E. and Aris, J.P.					
TITLE	Molecular analysis of mercury-induced antinuclear antibodies in					

RESULT 2	AY090903	AY090903	420 bp	mRNA	linear	ROD 17-APR-2002
LOCUS						
DEFINITION		Mus musculus clone GN-2-M4 monoclonal anti-alpha-1,3-galactosyltransferase IGM heavy chain mRNA, partial cds.				

## RESULT 3

AX458152  
LOCUS AX458152  
DEFINITION Sequence 15 from Patent WO0246237.  
ACCESSION AX458152  
VERSION AX458152.1 GI:21724902

## KEYWORDS

Mus musculus (house mouse)

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 Basi, G., Saldanha, J. and Yednock, T.

Humanized antibodies that recognize beta amyloid peptide

Patent: WO 0246237-A 15 13-JUN-2002;

Neuralab Limited (BM); Wyeth (US)

## JOURNAL

Neuralab Limited (BM); Wyeth (US)

## FEATURES

Location/Qualifiers

1..426

/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

1..>426

/note="unnamed protein product"

/codon\_start=1

/protein\_id="CAD38347.1"

/db\_xref="GI:21724903"

/translation="MDRLTSSFLLLIVPAVLQSOATLKESGPGILQSSOTLSITCSFS

GFSLSTSGMGVSVIROPKGLKLELAHIWDDDKRPNPSLKSRLITSKDTSRKQVFLK

ITSVDPADYATYCVRRPTPLVLDAMDVGQGTSTVSS"

1..57

sig\_peptide 94 a 119 c 101 g 112 t

BASE COUNT 94 a 119 c 101 g 112 t

ORIGIN

Query Match 85.9%; Score 311.8; DB 6; Length 426;

Best Local Similarity 92.4%; Pred. No. 6e-90;

Matches 341; Conservative 0; Mismatches 22; Indels 6; Gaps 1;

QY 1 CAGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60

DB 58 CAGGCTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 117

QY 61 ACTTGTCTTCTCTGGTCTTCTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 120

DB 118 ACTTGTCTTCTCTGGTCTTCTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 177

QY 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCCACACATTTTACTGGGATGATGACAAAGCGC 180

DB 178 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCCACACATTTTACTGGGATGATGACAAAGCGC 237

QY 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCACCAGGTA 240

DB 238 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCACCAGGTA 297

QY 241 TTCTCTCAAGATCAACAGTGTGGACACTCGAGATACCTCCACATCTGCTGCTCAAGG 300

DB 298 TTCTCTCAAGATCAACAGTGTGGACACTCGAGATACCTCCACATCTGCTGCTCAAGG 357

QY 301 GTC-----TCTTAAGTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 354

DB 358 CCAATTACTCCGGTACTAGTCTGATGCTATGCTATGCTATGCTATGCTATGCTATGCT 417

QY 355 GTCTCCCTCA 363

DB 418 GTCTCCCTCA 426

## RESULT 4

MMU22977  
LOCUS MMU22977  
DEFINITION Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,  
clone 45-11h, partial cds.

## ACCESSION

U22977

## VERSION

U22977.1 GI:780556

## KEYWORDS

Mus musculus (house mouse)

## SOURCE

Mus musculus

## ORGANISM

Mus musculus

## REFERENCE

1 (bases 1 to 360)

Young, D. and Kearney, J.F.

Sequence analysis and antigen binding characteristics of Ig SCID

Ig+ mice

Int. Immunol. 7 (5), 807-819 (1995)

PUBMED 7547707

2 (bases 1 to 360)

Young, D.C.

Direct Submission

Submitted (17-MAR-1995) David C. Young, University of Texas Health

Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,

Houston, TX 77030, USA

Location/Qualifiers

1..360

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CB17 SCID"

/sub\_species="domesticus"

/db\_xref="taxon:10090"

/clones="45-11h"

/cell\_type="lymphocyte"

/tissue\_type="spleen"

<1..>360

/codon\_start=1

/product="immunoglobulin heavy chain"

/protein\_id="AA096358.1"

/db\_xref="GI:780557"

/translation="QVTLKESGPGILQSSOTLSITCSFSGLSTSGMGVSVIROPKGLKLELAHIWDDDKRPNPSLKSRLITSKDTSRKQVFLK

GSSIFYWQGTTLTVSS"

BASE COUNT 84 a 97 c 87 g 92 t

ORIGIN

Query Match 84.1%; Score 305.4; DB 10; Length 360;

Best Local Similarity 92.0%; Pred. No. 7.2e-86;

Matches 334; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 CAGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60

DB 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60

QY 61 ACTTGTCTTCTCTGGGTTTCTCAGTCTGAGTCTTCTGATGGGTGTGAGTCTGATTCGA 120

DB 61 ACTTGTCTTCTCTGGGTTTCTCAGTCTGAGTCTTCTGATGGGTGTGAGTCTGATTCGT 120

QY 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCCACACATTTTACTGGGATGATGACAAAGCGC 180

DB 121 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCACCAGGTA 240

QY 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCACCAGGTA 240

DB 241 TTCTCTCAAGATCAACAGTGTGGACACTCGAGATACCTCCACATCTGCTGCTCAAGG 300

QY 301 GTC-----TCTTAAGTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 360

DB 301 GT---TCTAGTAGTAGTACTTTGACTACTTGGGGCCCAAGGCACCACTCTCACAGTCTCC 357

QY 361 TCA 363

DB 358 TCA 360

```
RESULT 5
MMU22979
LOCUS
DEFINITION
Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-12h, partial cds.
ACCESSION
U22979
VERSION
U22979.1 GI:780560
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 360)
Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
Ig+ mice
Int. Immunol. 7 (5), 807-819 (1995)
JOURNAL
MEDLINE
PUBMED
96053543
7547707
REFERENCE
2 (bases 1 to 360)
Young, D.C.
Direct Submission
Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
FEATURES
Location/Qualifiers
1..360
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-12h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>360
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AAA96360.1"
/db_xref="GI:780561"
/translations="QVTLKESGPGILQSSQTLSTLCSFSGFSLSTSGMGVSWIROPSPG
KGLEWLAIYWDKRYNPSLKRSLTISKDTSRQVFLKITSVDATATYTCARRVL
GSSYFDYWGQGTTLTVSS"
CDS
BASE COUNT 84 a 98 c 87 g 91 t
ORIGIN
Query Match 84.1%; Score 305.4; DB 10; Length 360;
Best Local Similarity 92.0%; Pred. No. 7.2e-88;
Matches 334; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Dy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Qy 61 ACTTGTTCTTCTCTGGGTTTTCATCAGCACATTCGATGGGTGTGAGCTGGATTGCA 120
Dy 61 ACTTGTTCTTCTCTGGGTTTTCATCAGCACATTCGATGGGTGTGAGCTGGATTGCA 120
Qy 121 CAGCCTTCAGAAAGGTCTGGAGTGTCTGGCTGGCACATTTACTTGGATGATGACAAGCG 180
Dy 121 CAGCCTTCAGAAAGGTCTGGAGTGTCTGGCTGGCACATTTACTTGGATGATGACAAGCG 180
Qy 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAAGGATACCTCCAGAACCCAGGTA 240
Dy 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAAGGATACCTCCAGAACCCAGGTA 240
Qy 241 TTCCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGCCACATCTACTGTGTGGAAG 300
Dy 241 TTCCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGCCACATCTACTGTGTGGAAG 300
Qy 301 GTCTCTCTACTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 360
Dy 301 GTCTCTCTACTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 360

301 G---CTCTAGTAGTAGCTACTTTTGACTACTGGGGCCAGGCAACCACTCTCAGACTCTCC 357
361 TCA 363
358 TCA 360

RESULT 6
MMU22994
LOCUS
DEFINITION
Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
clone 45-27h, partial cds.
ACCESSION
U22994
VERSION
U22994.1 GI:780590
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 360)
Young, D. and Kearney, J.F.
Sequence analysis and antigen binding characteristics of Ig SCID
Ig+ mice
Int. Immunol. 7 (5), 807-819 (1995)
JOURNAL
MEDLINE
PUBMED
96053543
7547707
REFERENCE
2 (bases 1 to 360)
Young, D.C.
Direct Submission
Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
FEATURES
Location/Qualifiers
1..360
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-27h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>360
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AAA96375.1"
/db_xref="GI:780591"
/translations="QVTLKESGPGILQSSQTLSTLCSFSGFSLSTSGMGVSWIROPSPG
KGLEWLAIYWDKRYNPSLKRSLTISKDTSRQVFLKITSVDATATYTCARRVL
GSSYFDYWGQGTTLTVSS"
CDS
BASE COUNT 84 a 95 c 87 g 94 t
ORIGIN
Query Match 84.1%; Score 305.4; DB 10; Length 360;
Best Local Similarity 92.0%; Pred. No. 7.2e-88;
Matches 334; Conservative 0; Mismatches 26; Indels 3; Gaps 1;
Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Dy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Qy 61 ACTTGTTCTTCTCTGGGTTTTCATCAGCACATTCGATGGGTGTGAGCTGGATTGCA 120
Dy 61 ACTTGTTCTTCTCTGGGTTTTCATCAGCACATTCGATGGGTGTGAGCTGGATTGCA 120
Qy 121 CAGCCTTCAGAAAGGTCTGGAGTGTCTGGCTGGCACATTTACTTGGATGATGACAAGCG 180
Dy 121 CAGCCTTCAGAAAGGTCTGGAGTGTCTGGCTGGCACATTTACTTGGATGATGACAAGCG 180
Qy 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAAGGATACCTCCAGAACCCAGGTA 240
Dy 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAAGGATACCTCCAGAACCCAGGTA 240
```



```

QY 241 TTCTCAAGATCACCAGTGTGGACACTCGAGATACGCCACATACACTACTGTGTCTGAAGG 300
Db 241 TTCTCAAGATCACCAGTGTGGACACTCGAGATACGCCACATACACTACTGTGTCTGAAGG 300
QY 301 GTCTCTTAAGTACCTAGTGTGGACACTCGAGATACGCCACATACACTACTGTGTCTGAAGG 300
Db 301 GTCTCTTAAGTACCTAGTGTGGACACTCGAGATACGCCACATACACTACTGTGTCTGAAGG 300
QY 361 TCA 363
Db 358 TCA 360

RESULT 7
MMU22992
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-26h, partial cds.
ACCESSION U22992
VERSION U22992
KEYWORDS U22992.1 GI:780586
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 360)
AUTHORS Young,D. and Kearney,J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young,D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
FEATURES
source
1..360
/mol_type="mRNA"
/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-26h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>360
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA056373.1"
/db_xref="GI:780586"
/translations="QVILKESGPIQLQSSQTSLTCSFSGSLSTSGMGSVNIQPSG
KGLWLAHYWDKRYNFKSLRSLFISKDTRNQVFLKITSVDATATYYCARRAL
GSTYFDYWGQGTTLTVSS"
BASE COUNT 83 a 99 c 87 g 91 t
ORIGIN
Query Match 83.7%; Score 303.8; DB 10; Length 360;
Best Local Similarity 91.7%; Pred. No. 2.4e-87;
Matches 333; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 CAGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Db 1 CAGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCTCTCCAGACCCCTCAGTCTG 60
QY 61 ACTTGTCTTTCTCGGGTTTTCATGAGCACTTCTGGTATGGGTGTGAGCTGGATTGCA 120
Db 61 ACTTGTCTTTCTCGGGTTTTCATGAGCACTTCTGGTATGGGTGTGAGCTGGATTGCT 120
QY 121 CAGCCTTCAGAAAGGCTCGGAGTGGCGCACATTTACTGGGATGATGACAGCGC 180

```

```

Db 121 CAGCCTTCAGAAAGGCTCGGAGTGGCGCACATTTACTGGGATGATGACAGCGC 180
QY 181 TATAACCCATCCCTGAAGAGCGCGCTTACATCTCCAGGATACCTCCAGCAACCAAGTA 240
Db 181 TATAACCCATCCCTGAAGAGCGCGCTTACATCTCCAGGATACCTCCAGCAACCAAGTA 240
QY 241 TTCTCTAAGATCACCAGTGTGGACACTCGAGATACGCCACATACACTACTGTGTCTGAAGG 300
Db 241 TTCTCTAAGATCACCAGTGTGGACACTCGAGATACGCCACATACACTACTGTGTCTGAAGG 300
QY 301 GTCTCTTAAGTACCTAGTGTGGACACTCGAGATACGCCACATACACTACTGTGTCTGAAGG 300
Db 301 GTCTCTTAAGTACCTAGTGTGGACACTCGAGATACGCCACATACACTACTGTGTCTGAAGG 300
QY 361 TCA 363
Db 358 TCA 360

RESULT 8
E07584
LOCUS Gene fragment coding the variable region in the heavy chain.
DEFINITION E07584
ACCESSION E07584
VERSION E07584.1 GI:2175719
KEYWORDS JP 1994141885-A/1.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 366)
AUTHORS Eda,Y., Nagatomi,K., Shiosaki,K., Maeda,H., Kurumi,K. and
Tokiyoshi,Y.
TITLE MONOCLONAL ANTIBODY
JOURNAL Patent: JP 1994141885-A 1 24-MAY-1994;
COMMENT CHEMO SERO THERAPEUT RES INST
OS Mus sp. (mouse)
PN JP 1994141885-A/1
PD 24-MAY-1994 JP 1992322476
PF 05-NOV-1992 JP 1992322476
PI ED A YASUYUKI, NAGATOMI KIYOSHI, SHIOSAKI KOUICHI, PI MAEDA
HIROAKI,
PI KURUMI KAZUHIKO, TOKIYOSHI YUKIO
PC C12P21/08.C07K15/28//C12N15/06.C12N15/13.C12N15/62.G01N33/569,
PC G01N33/577,
PC C12P21/08.C12R1:91;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..366
FT /organism="Mus sp."
FT /mol_type="genomic RNA"
FT /db_xref="taxon:10095"
BASE COUNT 85 a 98 c 84 g 99 t
ORIGIN
Query Match 83.6%; Score 303.6; DB 6; Length 366;
Best Local Similarity 91.3%; Pred. No. 2.8e-87;
Matches 334; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 CAGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Db 1 CAGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
QY 61 ACTTGTCTTTCTCGGGTTTTCATGAGCACTTCTGGTATGGGTGTGAGCTGGATTGCA 120
Db 61 ACTTGTCTTTCTCGGGTTTTCATGAGCACTTCTGGTATGGGTGTGAGCTGGATTGCT 120
QY 121 CAGCCTTCAGAAAGGCTCGGAGTGGCGCACATTTACTGGGATGATGACAGCGC 180

```

```

Db      121 CAGCCTTCAGGAAGGTTCTGGAGTGGCTGGGACACATTTATTGGGATGATGACAGAC 180
QY      181 TATAACCCATCCCTGAAGACCGGTTACATCTCAAGATACCTCCAGCAACAGGTA 240
Db      181 TATAACCCATCCCTGAAGACCGGTTACATCTCAAGATACCTCCAGCAACAGGTA 240
QY      241 TTCTCAAGATCACCAGTGTGACACTGCGACATCTGCGACATCTGCTCGAAGG 300
Db      241 TTCTCAAGATCACCAGTGTGACACTGCGACATCTGCGACATCTGCTCGAAGG 300
QY      301 G---TCTCTTAACCTCCATGCTATGGACTACTGGGTCAAGGAACCTCAGTACCGTC 357
Db      301 GTCTTCTATGTAACCTCCGATTTATGGACCACTGGGTCAAGGAACCTCAGTACCGTC 360
QY      358 TCCTCA 363
Db      361 TCCTCA 366

RESULT 9
MMU22981
LOCUS   Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION
ACCESSION U22981
VERSION   U22981.1 GI:780564
KEYWORDS
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 360)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL   Young,D. and Kearney,J.F.
MEDLINE   Sequence analysis and antigen binding characteristics of Ig SCID
PUBMED    96053543
REFERENCE 2 (bases 1 to 360)
AUTHORS   Ig+ mice
TITLE      Int. Immunol. 7 (5), 807-819 (1995)
JOURNAL   Young,D.C.
MEDLINE   Direct Submission
PUBMED    Submitted (17-MAR-1995) David C. Young, University of Texas Health
REFERENCE 2 (bases 1 to 360)
AUTHORS   Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
TITLE      Houston, TX 77030, USA
JOURNAL   Location/Qualifiers
FEATURES  source
           1..360
           /organism="Mus musculus"
           /mol_type="mRNA"
           /strain="CB17 SCID"
           /sub_species="domesticus"
           /db_xref="taxon:10090"
           /clone="45-13h"
           /cell_type="lymphocyte"
           /tissue_type="spleen"
           <1..>360
           /codon_start=1
           /product="immunoglobulin heavy chain"
           /protein_id="AA096362.1"
           /db_xref="GI:780565"
           /translation="QVTLKESGFGILQSSQTLSLTCSFGSFLSTSGMVSWIROPFG
           KGLEWLTHTIYWDGDKRYNPSLKRITISKDTSRNOVFLRITSVDTADTATYYCARRAL
           GSTVFDYWGQGTTLTVSS"
           GSTVFDYWGQGTTLTVSS"
CDS
BASE COUNT 83 a 99 c 87 g 91 t
ORIGIN
Query Match 82.8%; Score 300.6; DB 10; Length 360;
Best Local Similarity 91.2%; Pred.No.2.6e-86;
Matches 331; Conservative 0; Mismatches 29; Indels 3; Gaps 1;
QY      1 CAGCTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60
Db      1 CAGCTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCTTCCAGACCCCTCAGTCTG 60

```

```

QY      61 ACTTGTTCTTCTCTGGGTTTTCAGTGAGCATTCTGGTATGGGTGTGAGCTGGATTCA 120
Db      61 ACTTGTTCTTCTCTGGGTTTTCAGTGAGCATTCTGGTATGGGTGTGAGCTGGATTCT 120
QY      121 CAGCCTTCAGGAAGGTTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAGCG 180
Db      121 CAGCCTTCAGGAAGGTTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAGCG 180
QY      181 TATAACCCATCCCTGAAGACCGGTTTACAATCTCAAGGATACCTCCAGCAACAGGTA 240
Db      181 TATAACCCATCCCTGAAGACCGGTTTACAATCTCAAGGATACCTCCAGCAACAGGTA 240
QY      241 TTCTCAAGATCACCAGTGTGACACTCGAGATATCTGCCACATATCTGTGTCGAAGG 300
Db      241 TTCTCAAGATCACCAGTGTGACACTCGAGATATCTGCCACATATCTGTGTCGAAGG 300
QY      301 GTCTTCTTAACCTCCATGCTATGGACTACTGGGTCAAGGAACCTCAGTACCGCTCTCC 360
Db      301 G---CTCTAGGTAGTACTTGTGACTCTGGGCGCAAGGACCACTCTCAGCTCTCC 357
QY      361 TCA 363
Db      358 TCA 360

RESULT 10
MMU23010
LOCUS   Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION
ACCESSION U23010
VERSION   U23010.1 GI:780622
KEYWORDS
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 360)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL   Young,D. and Kearney,J.F.
MEDLINE   Sequence analysis and antigen binding characteristics of Ig SCID
PUBMED    96053543
REFERENCE 2 (bases 1 to 360)
AUTHORS   Ig+ mice
TITLE      Int. Immunol. 7 (5), 807-819 (1995)
JOURNAL   Young,D.C.
MEDLINE   Direct Submission
PUBMED    Submitted (17-MAR-1995) David C. Young, University of Texas Health
REFERENCE 2 (bases 1 to 360)
AUTHORS   Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
TITLE      Houston, TX 77030, USA
JOURNAL   Location/Qualifiers
FEATURES  source
           1..360
           /organism="Mus musculus"
           /mol_type="mRNA"
           /strain="CB17 SCID"
           /sub_species="domesticus"
           /db_xref="taxon:10090"
           /clone="45-6h"
           /cell_type="lymphocyte"
           /tissue_type="spleen"
           <1..>360
           /codon_start=1
           /product="immunoglobulin heavy chain"
           /protein_id="AA065401.1"
           /db_xref="GI:780623"
           /translation="QVTLKESGFGILQSSQTLSLTCSFGSFLSTSGMVSWIROPFG
           KGLEWLTHTIYWDGDKRYNPSLKRITISKDTSRNOVFLRITSVDTADTATYYCARRAL
           GSTVFDYWGQGTTLTVSS"
           GSTVFDYWGQGTTLTVSS"
CDS
BASE COUNT 83 a 99 c 87 g 91 t
ORIGIN
Query Match 82.8%; Score 300.6; DB 10; Length 360;

```

```
Best Local Similarity 91.2%; Pred. No. 2.6e-86;
Matches 331; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
QY 61 ACTTGTCTCTTCTCTGGGTTTTCACGTGACACTTCTGGTATGGGTGAGTGGATTCGA 120
DB 61 ACTTGTCTCTTCTCTGGGTTTTCACGTGACACTTCTGGTATGGGTGAGTGGATTCGT 120
QY 121 CAGCCTTCAGGAAAGGTTCTGAGTGGCTGGACACATTTACTGGGATGATGACAAGCGC 180
DB 121 CAGCCTTCAGGAAAGGTTCTGAGTGGCTGGACACATTTACTGGGATGATGACAAGCGC 180
QY 181 TATAACCCATCCTGAAGAGCGGCTTCAACTCCAGGATACCTCCAGCAACAGGTA 240
DB 181 TATAACCCATCCTGAAGAGCGGCTTCAACTCCAGGATACCTCCAGCAACAGGTA 240
QY 241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTCTCGAAG 300
DB 241 TTCCTCAGGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTCTCGAAG 300
QY 301 GTCTCTTAACCTCCATGCTATGACTACTGGGTCAAGGAACTCAGTACCGTCTCC 360
DB 301 G---CTCTAGGTAGTACCTACTTTGACTACTGGGCGCAAGCACCACCTCCTCAGTCTCC 357
QY 361 TCA 363
DB 358 TCA 360

RESULT 11
MMU23013 360 bp mRNA linear ROD 20-SEP-2001
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-8h, partial cds.
ACCESSION U23013
VERSION U23013.1 GI:780628
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 360)
AUTHORS Young, D. and Kearney, J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
FEATURES
source
1..360
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-8h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>360
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA65404.1"
/db_xref="GI:780628"
/translation="QVTLKESGFGILQSSQTLSTLCSFGSLSTSGMGVSWIRQPSG

CDS
KGLWLTHTLYWDGDKYENBLSRLTISKDTSRNOVFLRITSVDITADTATYYCARRAL
GSTYFDYWGQGTTLTVSS"
BASE COUNT 83 a 99 c 87 g 91 t
ORIGIN
Query Match 82.8%; Score 300.6; DB 10; Length 360;
Best Local Similarity 91.2%; Pred. No. 2.6e-86;
Matches 331; Conservative 0; Mismatches 29; Indels 3; Gaps 1;
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
QY 61 ACTTGTCTCTTCTCTGGGTTTTCACGTGACACTTCTGGTATGGGTGAGTGGATTCGA 120
DB 61 ACTTGTCTCTTCTCTGGGTTTTCACGTGACACTTCTGGTATGGGTGAGTGGATTCGT 120
QY 121 CAGCCTTCAGGAAAGGTTCTGAGTGGCTGGACACATTTACTGGGATGATGACAAGCGC 180
DB 121 CAGCCTTCAGGAAAGGTTCTGAGTGGCTGGACACATTTACTGGGATGATGACAAGCGC 180
QY 181 TATAACCCATCCTGAAGAGCGGCTTCAACTCCAGGATACCTCCAGCAACAGGTA 240
DB 181 TATAACCCATCCTGAAGAGCGGCTTCAACTCCAGGATACCTCCAGCAACAGGTA 240
QY 241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTCTCGAAG 300
DB 241 TTCCTCAGGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTCTCGAAG 300
QY 301 GTCTCTTAACCTCCATGCTATGACTACTGGGTCAAGGAACTCAGTACCGTCTCC 360
DB 301 G---CTCTAGGTAGTACCTACTTTGACTACTGGGCGCAAGCACCACCTCCTCAGTCTCC 357
QY 361 TCA 363
DB 358 TCA 360

RESULT 12
MMU23004 361 bp mRNA linear ROD 20-SEP-2001
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-3h, partial cds.
ACCESSION U23004
VERSION U23004.1 GI:780610
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 361)
AUTHORS Young, D. and Kearney, J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 361)
AUTHORS Young, D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
FEATURES
source
1..361
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-3h"
/cell_type="lymphocyte"
/tissue_type="spleen"
```

CDS

```

<1..>361
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA65395.1"
/db_xref="GI:780611"
/translation="OVTLKESGPGILQSSQTLSTLTCSPGSLSTSGMGSWIRQPSG
KGLEWLTHIYNDGDKYNPFLSKRLTISKDTSRNQVFLRITSVDTADTATYCCARRAL
GSTYFDYWGQGTTLTVSS"
BASE COUNT 83 a 99 c 88 g 91 t
ORIGIN

```

```

Query Match 82.8%; Score 300.6; DB 10; Length 361;
Best Local Similarity 91.2%; Pred. No. 2.6e-86;
Matches 331; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
DB 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGTCTCCAGACCCCTCAGTCTG 60
QY 61 ACTTGTTCTTTCTCTGGGTTTTCACCTGAGCATTCTGGTATGGGTGTGAGCTGGATTCTGA 120
DB 61 ACTTGTTCTTTCTCTGGGTTTTCACCTGAGCATTCTGGTATGGGTGTGAGCTGGATTCTG 120
QY 121 CAGCCTTCAGAAAGGCTCGAGTGGCTGGACACATTACTGGGATGATGACAAAGCGC 180
DB 121 CAGCCTTCAGAAAGGCTCGAGTGGCTGGACACATTACTGGGATGATGACAAAGCGC 180
QY 181 TATAACCCATCCTCGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACACAGGTA 240
DB 181 TATAACCCATCCTCGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACACAGGTA 240
QY 241 TTCCTCAAGATACCAAGTGTGACACTCGAGATATGCGCACATATCTGTGCTCGAAGG 300
DB 241 TTCCTCAGATACCAAGTGTGACACTCGAGATATGCGCACATATCTGTGCTCGAAGG 300
QY 301 GTCTCTCAAGTCCCTATGCTATGGACTACTGGGTCAGAGAACCTCAGTCAACCTCTCC 360
DB 301 G---CTCTAGGTAGTACCTACTTTGACTTCTGGGCGCAAGGACCACTCTCAGTCTCC 357
QY 361 TCA 363
DB 358 TCA 360

```

```

RESULT 13
MMU22999
LOCUS Mus musculus CB17 SCID immunoglobulin heavy chain V region mRNA,
DEFINITION clone 45-2h, partial cds.
ACCESSION U22999
VERSION U22999.1 GI:780600
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 360)
AUTHORS Young,D. and Kearney,J.F.
TITLE Sequence analysis and antigen binding characteristics of Ig SCID
JOURNAL Int. Immunol. 7 (5), 807-819 (1995)
MEDLINE 96053543
PUBMED 7547707
REFERENCE 2 (bases 1 to 360)
AUTHORS Young,D.C.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) David C. Young, University of Texas Health
Science Center, Houston, Pathology, 6431 Fannin, MSMB 2.137,
Houston, TX 77030, USA
FEATURES
source
1..360
/organism="Mus musculus"
/mol_type="mRNA"

```

```

/strain="CB17 SCID"
/sub_species="domesticus"
/db_xref="taxon:10090"
/clone="45-2h"
/cell_type="lymphocyte"
/tissue_type="spleen"
<1..>360
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA65390.1"
/db_xref="GI:780601"
/translation="OVTLKESGPGILQSSQTLSTLTCSPGSLSTSGMGSWIRQPSG
KGLEWLTHIYNDGDKYNPFLSKRLTISKDTSRNQVFLRITSVDTADTATYCCARRAL
GSTYFDYWGQGTTLTVSS"
BASE COUNT 82 a 99 c 87 g 92 t
ORIGIN

```

```

Query Match 82.5%; Score 299.6; DB 10; Length 360;
Best Local Similarity 91.2%; Pred. No. 5.6e-86;
Matches 330; Conservative 0; Mismatches 29; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
DB 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGTCTCCAGACCCCTCAGTCTG 60
QY 61 ACTTGTTCTTTCTCTGGGTTTTCACCTGAGCATTCTGGTATGGGTGTGAGCTGGATTCTGA 120
DB 61 ACTTGTTCTTTCTCTGGGTTTTCACCTGAGCATTCTGGTATGGGTGTGAGCTGGATTCTG 120
QY 121 CAGCCTTCAGAAAGGCTCGAGTGGCTGGACACATTACTGGGATGATGACAAAGCGC 180
DB 121 CAGCCTTCAGAAAGGCTCGAGTGGCTGGACACATTACTGGGATGATGACAAAGCGC 180
QY 181 TATAACCCATCCTCGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACACAGGTA 240
DB 181 TATAACCCATCCTCGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACACAGGTA 240
QY 241 TTCCTCAAGATACCAAGTGTGACACTCGAGATATGCGCACATATCTGTGCTCGAAGG 300
DB 241 TTCCTCAGGATACCAAGTGTGACACTCGAGATATGCGCACATATCTGTGCTCGAAGG 300
QY 301 GTCTCTCTAACTGCTATGCTATGGACTACTGGGTCAGAGAACCTCAGTCAACCTCTCC 360
DB 301 G---CTCTAGGTAGTACCTACTTTGACTTCTGGGCGCAAGGACCACTCTCAGTCTCC 357
QY 361 TC 362
DB 358 TC 359

```

```

RESULT 14
E07990
LOCUS DNA encoding inhibitor of binding IL-6 to its receptor.
DEFINITION E07990
ACCESSION E07990
VERSION E07990.1 GI:2176121
KEYWORDS JP 1994237772-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 738)
AUTHORS Shimamura,T., Nakazawa,H. and Hamuro,J.
TITLE IMMUNOSUPPRESSANT
JOURNAL Patent: JP 1994237772-A 1 30-AUG-1994;
AJINOMOTO CO INC
COMMENT
OS Unknown
PN JP 1994237772-A/1
PD 30-AUG-1994
PF 17-FEB-1993 JP 1993028173
PI SHIMAMURA TOSHIKI, NAKAZAWA HARUMI, HAMURO JUNJI PC
C12N15/12,A61K37/02,A61K37/02,C12N15/70,C12P21/02; CC
strandedness: Double;
CC topology: Linear;

```

EH Key Location/Qualifiers

FT source 1..738  
/organism='Unclassified'  
/cell\_type='hybridoma'  
/clone='HH61-10'  
FT mat\_peptide 1..738  
/product='inhibitor of binding og IL-6 to its  
receptor'.  
FT

FEATURES

source Location/Qualifiers  
1..738  
/organism='unidentified'  
/mol\_type='genomic RNA'  
/db\_xref='taxon:32644'  
BASE COUNT 187 a 189 c 180 g 182 t  
ORIGIN

Query Match 82.4%; Score 299.2; DB 6; Length 738;  
Best Local Similarity 90.1%; Pred. No. 7.6e-86;  
Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 367 CAGGTCAACTCGAGGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 426  
QY 61 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGGA 120  
DB 427 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGCT 486  
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGGC 180  
DB 487 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGGC 180  
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240  
DB 547 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240  
QY 241 TTCTCAAGATCAGAGTGGGACACTCGAGATCTGCCACATCTACTGTGCTCGAAG- 299  
DB 607 TTCTCAAGATCAGAGTGGGACACTCGAGATCTGCCACATCTACTGTGCTCGAAG- 299  
QY 300 -----GGTCTCTTAACCTGCTATGCTATGGACTACTGGGTCAAGGAACCTCAGTC 351  
DB 667 AGTCTCTATGGTATTGGGGGACTATGCTATGAGTACTGGGGTCAAGGAACCTCAGTC 726  
QY 352 ACCGTCCTCTCA 363  
DB 727 ACCGTCCTCTCA 738

RESULT 15  
LOCUS I45910 738 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 6 from patent US 5639455.  
ACCESSION I45910  
VERSION I45910.1 GI:2469875  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 738)  
AUTHORS Shimamura,T., Nakazawa,H. and Hamuro,J.  
TITLE Immunosuppressant  
JOURNAL Patent: US 5639455-A 6 17-JUN-1997;  
FEATURES Location/Qualifiers  
source 1..738  
/organism='unknown'  
BASE COUNT 187 a 189 c 180 g 182 t  
ORIGIN

Query Match 82.4%; Score 299.2; DB 6; Length 738;  
Best Local Similarity 90.1%; Pred. No. 7.6e-86;  
Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 367 CAGGTCAAACTCGAGGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 426  
QY 61 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGGA 120  
DB 427 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGCT 486  
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGGC 180  
DB 487 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAC 546  
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240  
DB 547 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240  
QY 241 TTCTCAAGATCAGAGTGGGACACTCGAGATCTGCCACATCTACTGTGCTCGAAG- 299  
DB 607 TTCTCAAGATCAGAGTGGGACACTCGAGATCTGCCACATCTACTGTGCTCGAAG- 299  
QY 300 -----GGTCTCTTAACCTGCTATGCTATGGACTACTGGGTCAAGGAACCTCAGTC 351  
DB 667 AGTCTCTATGGTATTGGGGGACTATGCTATGAGTACTGGGGTCAAGGAACCTCAGTC 726  
QY 352 ACCGTCCTCTCA 363  
DB 727 ACCGTCCTCTCA 738

Search completed: January 14, 2004, 17:00:15  
Job time : 1797.1 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 14:23:59 ; Search time 186.476 Seconds  
(without alignments)  
5254.805 Million cell updates/sec

Title: US-09-759-112a-5

Perfect score: 363

Sequence: 1 caggttactctgaagatgc.....cctcagtcacgcgtctctccta 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_19Jun03.\*

```

1: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	363	100.0	363	24	AA48651
2	363	100.0	363	24	AA48652
3	313.4	86.3	483	16	AAQ83491
4	313.4	86.3	483	20	AAQ85885
5	313.4	86.3	483	20	AAQ79520
6	311.8	85.9	423	16	AAQ83492
7	311.8	85.9	423	20	AAQ85886
8	311.8	85.9	423	20	AAQ79542

9	311.8	85.9	426	24	ABSS9429	Mouse 10D5 VH gene
10	303.6	83.6	366	15	AAQ58709	Humanised Mab H-ch
11	299.2	82.4	738	15	AAQ70612	IL-6 binding inhib
12	296.4	81.7	360	17	AAQ09300	Murine anti-Protei
13	291	80.2	418	16	AAQ75889	Murine heavy chain
14	284.4	78.3	465	24	ABN84609	Anti-Streptococcus
15	283	78.0	1416	25	ABZ24639	Humanised 10D5 ant
16	283	78.0	3255	25	ABZ24641	Humanised 10D5 ant
17	282	77.7	1413	21	ABK11000	DNA encoding prote
18	269	74.1	354	21	AAK14500	DNA sequence #1 in
19	267	73.6	369	21	AAA99646	Mouse antibody 13G
20	261.8	72.1	429	15	AAQ64156	Sequence of mouse
21	250.8	69.1	812	14	AAQ37056	Rat immunoglobulin
22	250.8	69.1	812	14	AAQ37056	KM50 Rat immunoglob
23	250.8	69.1	812	14	AAQ37056	Rat immunoglobulin
24	250.8	69.1	812	14	AAQ37056	Rat immunoglobulin
25	249.2	68.7	812	15	AAQ45437	Rat activated immu
26	195.8	53.9	363	22	AAH42390	KM50 cell-derived
27	191.4	52.7	423	14	AAQ45597	Nucleotide sequenc
28	191.4	52.7	423	14	AAQ45597	Sequence encoding
29	191.4	52.7	423	20	AAZ23965	Antibody B17X2 VH
30	190.6	52.5	423	20	AAZ23965	Human B17X2 antibo
31	190.2	52.4	613	16	AAQ78943	Anti-HIV-1 gp120 a
32	185.4	51.1	418	16	AAQ75916	Human immunoglobul
33	185.4	51.1	1607	22	AAQ66519	Human immune syste
34	184.6	50.9	444	18	AAQ80181	Monoclonal antibod
35	183.8	50.6	418	16	AAQ75917	Anti-human IL-6 ch
36	181.2	49.9	546	16	AAQ78964	Human immunoglobul
37	181	49.9	437	21	AAZ42289	Human 5' EST isola
38	180.4	49.7	1558	25	ABX12861	DNA encoding monoc
39	180.2	49.6	397	22	ABA08554	Human anti-HIV gpl
40	179.8	49.5	400	21	AAC00033	Human secreted pro
41	172.6	47.5	630	16	AAQ78948	Human immunoglobul
42	171	47.1	423	16	AAQ83493	Humanized antibody
43	171	47.1	423	20	AAQ85887	Heavy chain variab
44	171	47.1	423	20	AAQ79516	Heavy chain coding
45	168.8	46.5	447	20	AAZ20406	IgG antibody 2.4.4

#### ALIGNMENTS

##### RESULT 1

AL48651  
ID AAL48651 standard; DNA; 363 BP.

XX AAL48651;

XX 11-OCT-2002 (first entry)

DE Murine Mab 1F7 heavy chain coding sequence.

XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;  
complementarity determining region; framework-determining region;  
KW FR; heavy chain; light chain; HIV infection; gene; ss.

OS Mus sp.

XX WO200255668-A2.

XX 18-JUL-2002.

PF 11-JAN-2002; 2002WO-US00927.

PR 11-JAN-2001; 2001US-0759112.

XX (IMMP-) IMMOPHERON INC.

XX Muller S, Kohler H;

XX WPI; 2002-590668/63.

PT New polynucleotide encoding a complementarity- or framework-determining

PT region of an anti-idiotypic antibody that binds to human or primate  
PT anti- human immunodeficiency virus (HIV) antibodies, for use in  
XX vaccines against HIV -  
PS Claim 10; Page 17; 27pp; English.  
XX The present invention relates to coding sequences of the murine 1F7  
CC anti-idiotypic antibody complementarity-determining region (CDR) or  
CC framework-determining region (FR). The antibody binds to human or primate  
CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the  
CC treatment of HIV infection. The present sequence is the 1F7 heavy chain  
XX coding sequence.  
XX Sequence 363 BP; 83 A; 100 C; 88 G; 92 T; 0 other;  
SQ  
Query Match 100.0%; Score 363; DB 24; Length 363;  
Best Local Similarity 100.0%; Pred. No. 7.7e-102;  
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 60  
DB 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 60  
QY 61 ACTGTCTCTTCTCTGGGTTTTCACAGACCTTCTGGTATGGGTGAGCTGGATTGGA 120  
DB 61 ACTGTCTCTTCTCTGGGTTTTCACAGACCTTCTGGTATGGGTGAGCTGGATTGGA 120  
QY 121 CAGCCCTTCAGGAAGCGTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCGC 180  
DB 121 CAGCCCTTCAGGAAGCGTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCGC 180  
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGGACCCAGGTA 240  
DB 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGGACCCAGGTA 240  
QY 241 TTCTCTCAAGATCACCAAGTCTGGACATCTGCACATCTGCTGCTCGAAGG 300  
DB 241 TTCTCTCAAGATCACCAAGTCTGGACATCTGCACATCTGCTGCTCGAAGG 300  
QY 301 GTCTCTTAAGTCCCTATGCTATGAGTCTGAGTCTGAGGTCAGGAACTTCAGTCAACCTCTCC 360  
DB 301 GTCTCTTAAGTCCCTATGCTATGAGTCTGAGTCTGAGGTCAGGAACTTCAGTCAACCTCTCC 360  
QY 361 TCA 363  
DB 361 TCA 363  
RESULT 2  
AAL48652 standard; DNA; 363 BP.  
XX AAL48652;  
XX 11-OCT-2002 (first entry)  
XX Murine Mab 1F7 heavy chain coding sequence.  
XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;  
XX complementarity determining region; framework-determining region;  
XX FR; heavy chain; light chain; HIV infection; gene; ss.  
XX Mus sp.  
XX Key Location/Qualifiers  
XX CDS 1..363  
XX /\*tag= a  
XX /product= "1F7 heavy chain"  
XX /partial  
XX /note= "no start or stop codon"  
XX WO200255658-A2.  
XX

PD 18-JUL-2002.  
XX  
XX 11-JAN-2002; 2002WO-US00927.  
XX  
XX 11-JAN-2001; 2001US-0759112.  
XX (IMMP-) IMPHERON INC.  
XX Muller S, Kohler H;  
XX WPI; 2002-590658/63.  
XX P-PSDB; AAC18528.  
XX  
XX New polynucleotide encoding a complementarity- or framework-determining  
XX region of an anti-idiotypic antibody that binds to human or primate  
XX anti- human immunodeficiency virus (HIV) antibodies, for use in  
XX vaccines against HIV -  
XX Disclosure; Page 17-18; 27pp; English.  
XX  
XX The present invention relates to coding sequences of the murine 1F7  
XX anti-idiotypic antibody complementarity-determining region (CDR) or  
XX framework-determining region (FR). The antibody binds to human or primate  
XX anti-human immunodeficiency virus (HIV) antibodies and can be used in the  
XX treatment of HIV infection. The present sequence is the 1F7 heavy chain  
XX coding sequence.  
XX Sequence 363 BP; 83 A; 100 C; 88 G; 92 T; 0 other;  
SQ  
Query Match 100.0%; Score 363; DB 24; Length 363;  
Best Local Similarity 100.0%; Pred. No. 7.7e-102;  
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 60  
DB 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 60  
QY 61 ACTGTCTCTTCTCTGGGTTTTCACAGACCTTCTGGTATGGGTGAGCTGGATTGGA 120  
DB 61 ACTGTCTCTTCTCTGGGTTTTCACAGACCTTCTGGTATGGGTGAGCTGGATTGGA 120  
QY 121 CAGCCCTTCAGGAAGCGTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCGC 180  
DB 121 CAGCCCTTCAGGAAGCGTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCGC 180  
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGGACCCAGGTA 240  
DB 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGGACCCAGGTA 240  
QY 241 TTCTCTCAAGATCACCAAGTCTGGACATCTGCACATCTGCTGCTCGAAGG 300  
DB 241 TTCTCTCAAGATCACCAAGTCTGGACATCTGCACATCTGCTGCTCGAAGG 300  
QY 301 GTCTCTTAAGTCCCTATGCTATGAGTCTGAGTCTGAGGTCAGGAACTTCAGTCAACCTCTCC 360  
DB 301 GTCTCTTAAGTCCCTATGCTATGAGTCTGAGTCTGAGGTCAGGAACTTCAGTCAACCTCTCC 360  
QY 361 TCA 363  
DB 361 TCA 363  
RESULT 3  
AAQ83491 standard; cDNA; 483 BP.  
XX AAQ83491  
XX AAQ83491;  
XX 25-MAR-2003 (updated)  
XX 20-SEP-1995 (first entry)  
XX Mouse Mab 3B9 heavy chain.  
XX

KW Chimeric antibody; humanized antibody; antibody engineering;  
 KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; ds.  
 XX

OS Mus sp.

XX Key Location/Qualifiers  
 FH 64..483  
 FT /\*tag= a  
 FT sig\_peptide 64..120  
 FT /\*tag= b  
 FT mat\_peptide 121..483  
 FT /\*tag= c

XX WO9507301-A1.

XX 16-MAR-1995.

XX 07-SEP-1994; 94WO-US10308.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;  
 XX WPI; 1995-123387/16.  
 XX P-PSDB; AAR70190.

XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 XX from high affinity mAbs - useful in treatment of IL-4-mediated  
 XX and IgE-mediated allergic conditions

XX Disclosure; Fig.2; 97pp; English.

XX Spleen cells from mice immunized with human IL-4 were used to prepare  
 XX hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
 XX clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
 XX chains were cloned into pGEM7f+ and transformed into E. coli  
 XX DH5-alpha. The clones were sequenced (AAQ83490-91), and used for  
 XX antibody engineering.  
 XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;

Query Match 86.3%; Score 313.4; DB 16; Length 483;  
 Best Local Similarity 91.5%; Pred. No. 1.6e-86;  
 Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGGTTACTCTGAAGAGCTGGCCCTGGGATTTGCAGCCCTCCGAGACCTCAGTCTG 60  
 DB 121 CAGGTTACTCTGAAGAGCTGGCCCTGGGATTTGCAGCCCTCCGAGACCTCAGTCTG 180  
 QY 61 ACTTGTCTTCTCTGGGTTTTCACATGACACTCTGGTATGGGTGATGCGATTGGA 120  
 DB 181 ACTTGTCTTCTCTGGGTTTTCACATGACACTCTGGTATGGGTGATGCGATTGGA 240  
 QY 121 CAGCCTTCAGGAAAGGCTTGAGTGGCTGGGACACATTACTTGGGATGATCAAGCGC 180  
 DB 241 CAGCCTTCAGGAAAGGCTTGAGTGGCTGGGACACATTACTTGGGATGATCAAGCGC 300  
 QY 181 TATAACCCATCCTGAAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 240  
 DB 301 TATAACCCATCCTGAAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 360  
 QY 241 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTCCACATCTACTGTCTCGAAG 300  
 DB 361 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTCCACATCTACTGTCTCGAAG 420  
 QY 301 GTCTCTCTACTGCCTATGCTATGACTACTGGGTCAGGAACTCAGTACCGTCTCC 360  
 DB 421 GAGACTGTCTTCTACTGGTACTTCGATGTCTGGGGCGCAGGACCAAGTCAACGTCCT 480

QY 361 TCA 363  
 DB 481 TCA 483

RESULT 4

AA85885  
 ID AAX85885 standard; CDNA; 483 BP.

XX AC AAX85885;

XX 13-SEP-1999 (first entry)

XX Heavy chain variable region cDNA of murine IL-4 antibody 3B9.

XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;  
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;  
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;  
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;  
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;  
 XX allergy; ds.

XX Mus sp.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;  
 XX WPI; 1999-429500/36.  
 XX P-PSDB; AAY23768.

XX New DNA molecules encoding recombinant antibodies useful for  
 XX treating IL4-mediated conditions

XX Claim 3; Fig 2; 50pp; English.

XX The present sequence encodes the heavy chain variable region of  
 CC murine interleukin-4 (IL-4) antibody 3B9. The sequences are used  
 CC in the production of chimeric and humanised IL-4 monoclonal antibodies.  
 CC The antibodies of the invention are used in therapeutic and  
 CC pharmaceutical compositions for treating IL-4 mediated and  
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,  
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,  
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.  
 CC They are also useful in the diagnosis of an allergy or condition  
 CC associated with excess IL-4 production through the measurement e.g. by  
 CC ELISA of circulating endogenous IL-4 levels in humans.

XX Sequence 483 BP; 108 A; 130 C; 124 G; 121 T; 0 other;

Query Match 86.3%; Score 313.4; DB 20; Length 483;  
 Best Local Similarity 91.5%; Pred. No. 1.6e-86;  
 Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 CAGGTTACTCTGAAGAGCTGGCCCTGGGATTTGCAGCCCTCCGAGACCTCAGTCTG 60

DB 121 CAGGTTACTCTGAAGAGCTGGCCCTGGGATTTGCAGCCCTCCGAGACCTCAGTCTG 180

QY 61 ACTTGTCTTCTCTGGGTTTTCACATGACACTCTGGTATGGGTGATGCGATTGGA 120





DR WPI; 1995-123387/16.  
 XX P-PSDB; AAR70191.  
 XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 XX Disclosure; Fig.3; 97pp; English.  
 XX A human/mouse chimeric antibody heavy chain variable region was  
 CC constructed (given in AAR70191) that contained the mouse anti-human  
 CC IL-4 MAb 3B9 variable region including 3 CDRs (AAR70198-200) and a  
 CC human antibody signal peptide (AAR70193). The construct was used  
 CC for humanized antibody production.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;  
 SQ

Query Match 85.9%; Score 311.8; DB 16; Length 423;  
 Best Local Similarity 91.2%; Pred. No. 4.8e-86;  
 Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
 Db 61 CAGGTTACCTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 120  
 QY 61 ACTTGTTCTTCTCTGGGTTTCACTGAGCATTCTCTGGTATGGGTGTGAGTTCGA 120  
 Db 121 ACTTGTTCTTCTCTGGGTTTCACTGAGCATTCTCTGGTATGGGTGTGAGTTCGT 180  
 QY 121 CAGCCTTCAGGAAGGTCTGGAGTGGCTGGCAGACATTTACTGGATGATGACAGCC 180  
 Db 181 CAGCCTTCAGGAAGGTCTGGAGTGGCTGGCAGACATTTACTGGATGATGACAGCC 240  
 QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 240  
 Db 241 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 300  
 QY 241 TTCTCTAAGATCACCAGTGTGGACACTGCGAGTACTGCGGCTCAAGCACTCAGTCC 360  
 Db 361 GAGACTGTGTTCTACTGGTACTTCGATGTCTGGGGCCGAGGACCGGTACCGTCTCC 420  
 QY 361 TCA 363  
 Db 421 TCA 423

RESULT 7  
 AAX85886  
 ID AAX85886 standard; cDNA; 423 BP.  
 XX AC AAX85886;  
 XX 13-SEP-1999 (first entry)  
 XX Heavy chain variable region cDNA of murine/human chimeric antibody 3B9.  
 XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;  
 XX chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;  
 XX immunoglobulin B-mediated allergic reaction; allergic rhinitis;  
 XX conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;  
 XX rheumatoid arthritis; host-versus-graft disease; renal disease;  
 XX allergy; ds.  
 XX Chimeric - Mus sp.  
 XX Chimeric - Homo sapiens.  
 XX US5928904-A.

PD 27-JUL-1999.  
 XX 07-JUN-1995; 95US-0483632.  
 XX 07-JUN-1995; 95US-0483632.  
 PR 07-SEP-1993; 93US-0117366.  
 PR 14-OCT-1993; 93US-0136783.  
 PR 07-SEP-1994; 94WO-US10308.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX Gross MS, Holmes SD, Sylvester DR;  
 XX WPI; 1999-429500/36.  
 DR P-PSDB; AAY23769.  
 XX New DNA molecules encoding recombinant antibodies useful for  
 PT treating IL4-mediated conditions  
 PT Example 3; Fig 3; 50pp; English.  
 XX The present sequence encodes the heavy chain variable region of  
 CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The  
 CC specification describes chimeric and humanised IL-4 monoclonal  
 CC antibodies. The antibodies of the invention are used in therapeutic  
 CC and pharmaceutical compositions for treating IL-4 mediated and  
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,  
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,  
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.  
 CC They are also useful in the diagnosis of an allergy or condition  
 CC associated with excess IL-4 production through the measurement e.g. by  
 CC ELISA of circulating endogenous IL-4 levels in humans.  
 XX Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;  
 SQ

Query Match 85.9%; Score 311.8; DB 20; Length 423;  
 Best Local Similarity 91.2%; Pred. No. 4.8e-86;  
 Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
 Db 61 CAGGTTACCTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 120  
 QY 61 ACTTGTTCTTCTCTGGGTTTCACTGAGCATTCTCTGGTATGGGTGTGAGTTCGA 120  
 Db 121 ACTTGTTCTTCTCTGGGTTTCACTGAGCATTCTCTGGTATGGGTGTGAGTTCGT 180  
 QY 121 CAGCCTTCAGGAAGGTCTGGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCC 180  
 Db 181 CAGCCTTCAGGAAGGTCTGGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCC 240  
 QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 240  
 Db 241 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 300  
 QY 241 TTCTCTAAGATCACCAGTGTGGACACTGCGAGTACTGCGGCTCAAGCACTCAGTCC 300  
 Db 301 TTCTCTAAGATCACCAGTGTGGACACTGCGAGTACTGCGGCTCAAGCACTCAGTCC 360  
 QY 301 GTCTCTTCTAAGTCTTCTACTGGTACTTCGATGTCTGGGGCCGAGGACCGGTACCGTCTCC 360  
 Db 361 GAGACTGTGTTCTACTGGTACTTCGATGTCTGGGGCCGAGGACCGGTACCGTCTCC 420  
 QY 361 TCA 363  
 Db 421 TCA 423

RESULT 8  
 AAX79542  
 ID AAX79542 standard; cDNA; 423 BP.  
 XX

AA79542;  
 11-AUG-1999 (first entry)  
 Chimeric 3B9 monoclonal antibody heavy chain coding sequence.  
 Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;  
 allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;  
 atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;  
 autoimmune disease; graft versus host disease; ss.  
 Synthetic.  
 US5914110-A.  
 22-JUN-1999.  
 07-JUN-1995; 95US-0483636.  
 07-JUN-1995; 95US-0483636.  
 07-SEP-1993; 93US-0117366.  
 14-OCT-1993; 93US-0136783.  
 07-SEP-1994; 94WO-US10308.  
 (SMK) SMITHKLINE BEECHAM CORP.  
 (SMK) SMITHKLINE BEECHAM PLC.  
 Gross MS, Holmes SD, Sylvester DR;  
 WPI: 1999-370482/31.  
 P-PSDB; AA18125.  
 Recombinant IL4 antibodies  
 Example 5; Fig 3; 50pp; English.  
 This sequence represents the DNA encoding the light chain of the  
 chimeric 3B9 antibody of the invention. The antibody is a chimeric or  
 humanised interleukin-4 (IL4) monoclonal antibody for the treatment of  
 immunoglobulin E (IGE) mediated diseases. The antibodies are useful for  
 the treatment of allergic disorders such as allergic rhinitis,  
 conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.  
 The antibodies are also useful for regulating B and T cell proliferation  
 and as such are useful in the treatment of autoimmune diseases and graft  
 versus host disease.  
 Sequence 423 BP; 87 A; 115 C; 110 G; 111 T; 0 other;  
 Query Match 85.9%; Score 311.8; DB 20; Length 423;  
 Best Local Similarity 91.2%; Pred. No. 4.8e-86;  
 Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
 1 CAGGTTACTGAAAGAGTCTGGCCCTGGGATTTGACGCTCCAGACCTCAGCTG 60  
 61 CAGGTTACTGAAAGAGTCTGGCCCTGGGATTTGACGCTCCAGACCTCAGCTG 120  
 61 ACTTGTTCTTCTCTGGTTTTCACGTAGACACTCTGGTATGGGTGAGCTGATCGA 120  
 121 ACTTGTTCTTCTCTGGTTTTCACGTAGACACTCTGGTATGGGTGAGCTGATCGT 180  
 121 CAGCCTTCAGGAAGGTTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGG 180  
 181 CAGCCTTCAGGAAGGTTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGG 240  
 181 TATAACCCATCCCTGAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 240  
 241 TATAACCCATCCCTGAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 300  
 241 TTCTCTCAAGATCAACGAGTGGGACACTTCAGAGATACGCCACATCTACTGTGCTG 300  
 301 TTCTCTCAAGATCAACGAGTGGGACACTTCAGAGATACGCCACATCTACTGTGCT 360  
 301 GTCTCTTAACCTGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTACCGTCTCC 360

361 GAGACTGTGTTCTACTGCTACTTGCATGTCCTGGGGCGGAGGACACCGTCTCC 420  
 361 TCA 363  
 421 TCA 423  
 RESULT 9  
 ABS59429 standard; DNA; 426 BP.  
 ABS59429;  
 05-NOV-2002 (first entry)  
 Mouse 10D5 VH gene.  
 Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;  
 variable region complementarity determining region; 3b6; 10D5;  
 variable framework region; amyloidogenic disease; Alzheimer's disease;  
 amyloid deposit; variable light chain; VL; variable heavy chain; VH;  
 notropic; neuroprotective; inhibitor of beta amyloid accumulation;  
 Abeta; gene; ds.  
 Mus musculus.  
 WO200246237-A2.  
 13-JUN-2002.  
 06-DEC-2001; 2001WO-US46587.  
 06-DEC-2000; 2000US-251892P.  
 (NEUR-) NEURALAB LTD.  
 (AMHP) WYETH.  
 Basi G, Saldanha J, Yednock T;  
 WPI: 2002-519658/55.  
 P-PSDB; ABG76934.  
 Novel light/heavy chain of humanized immunoglobulin for treating  
 amyloidogenic disease, has 3D6/10D5 variable region complementarity  
 determining regions and variable framework region from human acceptor  
 immunoglobulin -  
 Claim 151; Page 105; 171pp; English.  
 The present invention relates to new humanized immunoglobulin (Ig) light  
 chain (LC) or heavy chain (HC) comprising variable region complementarity  
 determining regions from 3D6/10D5 Ig LC or HC variable region sequence,  
 and variable framework region from human acceptor Ig LC or HC sequence.  
 The invention is useful for preventing or treating an amyloidogenic  
 disease or Alzheimer's disease in a patient. The invention is also useful  
 for in vivo imaging amyloid deposits in a patient. The present nucleic  
 acid sequence encodes a mouse 3D6/10D5 variable light (VL) chain or  
 variable heavy (VH) chain protein of the invention.  
 Sequence 426 BP; 94 A; 119 C; 101 G; 112 T; 0 other;  
 Query Match 85.9%; Score 311.8; DB 24; Length 426;  
 Best Local Similarity 92.4%; Pred. No. 4.8e-86;  
 Matches 341; Conservative 0; Mismatches 22; Indels 6; Gaps 1;  
 1 CAGGTTACTGAAAGAGTCTGGCCCTGGGATTTGACGCTCCAGACCTCAGCTG 60  
 58 CAGGTTACTGAAAGAGTCTGGCCCTGGGATTTGACGCTCCAGACCTCAGCTG 117  
 61 ACTTGTTCTTCTCTGGTTTTCACGTAGACACTCTGGTATGGGTGAGCTGATCGA 120  
 118 ACTTGTTCTTCTCTGGTTTTCACGTAGACACTCTGGTATGGGTGAGCTGATCGT 177

121 CAGCTTCAGGAAGGGTCTGGAGTGGCTGGACACATTTACTGGGATGATGACAGCGC 180  
 178 CAGCTTCAGGAAGGGTCTGGAGTGGCTGGACACATTTACTGGGATGATGACAGCGC 237  
 181 TATAAACCCTCCCTGAAGAGCGGCTTACAAATCTCCAAGGATACCTCCAGCAACAGGTA 240  
 238 TATAAACCCTCCCTGAAGAGCGGCTCACAATCTCCAAGGATACCTCCAGCAACAGGTA 297  
 241 TTCTCTCAGATCAGCAGTGTGGACATCTCGAGATGACTGCCATACCTACTGTGCTCGAAGG 300  
 298 TTCTCTCAGATCAGCAGTGTGGACATCTCGAGATGACTGCCATACCTACTGTGCTCGAAGG 357  
 301 GTC-----TCTCTAAGTCTGCTATGCTATGCTACTTGGGCTCAAGGAACTCAGTCACC 354  
 358 CCATTAATCTCGGTACTAGTCTGATGCTATGCTACTTGGGCTCAAGGAACTCAGTCACC 417  
 355 GTCTCTCA 363  
 418 GTCTCTCA 426

RESULT 10  
 AAQ68709  
 ID AAQ68709 standard; cDNA to mRNA; 366 BP.  
 AC AAQ68709;  
 XX  
 DT 08-FEB-1995 (first entry)  
 DE Humanised MAb H-chain coding sequence.  
 XX  
 KW Human; mouse; murine; heavy; light; chain; monoclonal; antibody;  
 KW complementarity determining region; CDR; IgG; kappa; IIIB; IIMN; ds.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 OS  
 PN JP06141885-A.  
 XX  
 PD 24-MAY-1994.  
 XX  
 PF 05-NOV-1992; 92JP-0322476.  
 XX  
 PR 05-NOV-1992; 92JP-0322476.  
 XX  
 PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
 XX  
 DR WPI; 1994-205040/25.  
 DR P-PSDB; AAR54101.  
 XX  
 PT Recombinant anti-HIV monoclonal antibody - capable of  
 PT neutralising strains which can not be neutralised by anti-IIIB  
 PT and IIMN antibodies  
 XX  
 PS Disclosure; Page 13; 23pp; Japanese.  
 XX  
 CC The sequences given in AAQ68709-10 encode the heavy and light chains  
 CC respectively of the humanised monoclonal antibody (MAb) of the  
 CC invention. The antibody has the ability to neutralise human  
 CC immunodeficiency virus. The antibody is classified as IgG kappa and  
 CC has the sequence RIGPKR or RYCPGR in the principal neutralising  
 CC domain. The antibody may be used to neutralise the clinically  
 CC separate strains which cannot be neutralised by the neutralising  
 CC antibodies against IIIB and IIMN strains.  
 XX  
 SQ Sequence 366 BP; 85 A; 98 C; 84 G; 99 T; 0 other;  
 Query Match 83.6%; Score 303.6; DB 15; Length 366;  
 Best Local Similarity 91.3%; Pred. No. 1.5e-83;  
 Matches 334; Conservative 0; Mismatches 29; Indels 3; Gaps 1;  
 1 CAGGTACTCTGAAGAGTCTGGCCCTGGTATATTGAGCCCTCCAGACCCCTCAGTCTG 60

1 CAGGTACTCTGAAGAGTCTGGCCCTGGTATATTGAGCCCTCCAGACCCCTCAGTCTG 60  
 61 ACTTGTCTTTCTCTGGGTTTTCATGAGCACATTTCTGGTATGGGTGTGAGCTGGATTGGA 120  
 61 ACTTGTCTTTCTCTGGGTTTTCATGAGCACATTTCTGGTATGGGTGTGAGCTGGATTGGA 120  
 121 CAGCTTCAGGAAGGGTCTGGAGTGGCTGGACACATTTACTGGGATGATGACAGCGC 180  
 121 CAGCTTCAGGAAGGGTCTGGAGTGGCTGGACACATTTATTGGGATGATGACAGCGC 180  
 181 TATAAACCCTCCCTGAAGAGCGGCTTACAAATCTCCAAGGATACCTCCAGCAACAGGTA 240  
 181 TATAAACCCTCCCTGAAGAGCGGCTCACAATCTCCAAGGATACCTCCAGCAACAGGTA 240  
 241 TTCTCTCAGATCAGCAGTGTGGACATCTCGAGATGACTGCCATACCTACTGTGCTCGAAGG 300  
 241 TTCTCTCAGATCAGCAGTGTGGACATCTCGAGATGACTGCCATACCTACTGTGCTCGAAGG 300  
 301 G---TCTCTCTAAGTCTGCTATGCTATGCTACTTGGGCTCAAGGAACTCAGTCACCGTC 357  
 301 GTCTCTATGCTAAGTCTGCTATGCTACTTGGGCTCAAGGAACTCAGTCACCGTC 357  
 358 TCCTCA 363  
 361 TCCTCA 366

RESULT 11  
 AAQ70612  
 ID AAQ70612 standard; DNA; 738 BP.  
 AC AAQ70612;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 28-APR-1995 (first entry)  
 XX  
 DE IL-6 binding inhibitor DNA.  
 XX  
 KW Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;  
 KW septic shock; multiple myeloma; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP617126-A2.  
 XX  
 PD 28-SEP-1994.  
 XX  
 PF 16-FEB-1994; 94EP-0102346.  
 XX  
 PR 17-FEB-1993; 93JP-0028173.  
 XX  
 PA (AJIN ) AJINOMOTO KK.  
 XX  
 PI Hamuro J, Nakazawa H, Shimamura T;  
 XX  
 DR WPI; 1994-295777/37.  
 DR P-PSDB; AAR58612.  
 XX  
 PT Polypeptide inhibiting binding of human interleukin-6 (IL-6) to  
 PT its receptor - useful for treating autoimmune disease induced  
 PT or aggravated by IL-6  
 XX  
 PS Claim 9; Page 19; 26pp; English.  
 XX  
 CC AAQ70612 codes for human interleukin-6 binding inhibitor, the  
 CC polypeptide described in AAR58612. This polypeptide inhibits the  
 CC binding of human IL-6 to its receptor, and can therefore be  
 CC useful in the treatment of a variety of autoimmune diseases;  
 CC specifically in the treatment of rheumatoid arthritis, septic  
 CC shock due to bacterial infection and multiple myeloma.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 738 BP; 187 A; 189 C; 180 G; 182 T; 0 other;  
 Query Match 82.4%; Score 299.2; DB 15; Length 738;  
 Best Local Similarity 90.1%; Pred. No. 4.4e-82;  
 Matches 335; Conservative 0; Mismatches 28; Indels 9; Gaps 1;  
 QY 1 CAGGTACTCTGAAGAGCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
 Db 367 CAGGTCAAACTCGAGAGCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 426  
 QY 61 ACTTGTCTTTCTCTGGTTTCTACAGACCTCTTGGTATGGGTGTAGCTGGATTGGA 120  
 Db 427 ACTTGTCTTTCTCTGGTTTCTACAGACCTCTTGGTATGGGTGTAGCTGGATTGGA 486  
 QY 121 CAGCCTTCAGGAAGAGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAGCGC 180  
 Db 487 CAGCCTTCAGGAAGAGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAGCGC 546  
 QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATTCGAAGGATACCTTCCAGCAACAGGTA 240  
 Db 547 TATAACCCATCCCTGAAGAGCCGGCTTACAATTCGAAGGATACCTTCCAGCAACAGGTA 606  
 QY 241 TTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGACATCTACTGTCTGGAAG- 299  
 Db 607 TTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGACATCTACTGTCTGGAAG- 666  
 QY 300 -----GGTCTCTCTAACTGGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTC 351  
 Db 667 AGTCTCTATGTAATTTGGGGGACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTC 726  
 QY 352 ACGTCTCTCTCA 363  
 Db 727 ACGTCTCTCTCA 738

RESULT 12  
 AAT09300  
 ID AAT09300 standard; DNA; 360 BP.  
 XX  
 AC AAT09300;  
 XX  
 DT 25-JUL-1996 (first entry)  
 XX  
 DE Murine anti-Protein C Mab HPC-4 VH gamma mature protein coding region.  
 XX  
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
 KW zymogen; cleavage; mouse; humanised antibody; variable region;  
 KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FN W09534652-A1.  
 XX  
 PD 21-DEC-1995.  
 XX  
 PF 09-JUN-1995; 95WO-US07372.  
 XX  
 PR 10-JUN-1994; 94US-0259321.  
 XX  
 PA (OKLA-) OKLAHOMA MED RES FOUND.  
 XX  
 PI Esmon CT, Rezaie A;  
 XX  
 DR WPI; 1996-049681/05.  
 XX  
 DR P-PSDB; AAR88109.  
 XX  
 FT Calcium-binding monoclonal antibody immunoreactive with Protein C -  
 FT inhibits Protein C anticoagulant activation by  
 FT thrombin-thrombomodulin, e.g. for treating tumours  
 XX  
 PS Claim 4; Page 30; 41pp; English.  
 XX  
 CC This is the nucleotide sequence encoding the mature protein from the

CC murine anti-protein C monoclonal antibody HPC-4 heavy chain variable  
 CC region (VH gamma). HPC-4 recognises the activation peptide region  
 CC (AAR88106) of the heavy chain of protein C, a vitamin K-dependent plasma  
 CC protein zymogen. Protein C is activated to activated protein C (APC)  
 CC by cleavage between the Arg-leu amino acid contained within the  
 CC activation peptide sequence. HPC-4 prevents protein C activation to  
 CC APC by binding to this region. The DNA sequences encoding the variable  
 CC regions of the heavy and light chains of the antibody (AAT09299-302)  
 CC were used to construct humanised antibodies using the PCR primers  
 CC AAT09303-9. The humanised antibodies are useful as inhibitors of  
 CC coagulation and can be used for the treatment of tumours by inhibiting  
 CC the anticoagulant activity of APC by preventing conversion of protein C  
 CC to APC.  
 XX  
 SQ Sequence 360 BP; 82 A; 91 C; 95 G; 92 T; 0 other;  
 Query Match 81.7%; Score 296.4; DB 17; Length 360;  
 Best Local Similarity 90.6%; Pred. No. 2.5e-81;  
 Matches 328; Conservative 0; Mismatches 31; Indels 3; Gaps 1;  
 QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
 Db 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
 QY 61 ACTTGTCTTTCTCTGGTTTCTACAGACCTCTTGGTATGGGTGTAGCTGGATTGGA 120  
 Db 61 ACTTGTCTTTCTCTGGTTTCTACAGACCTCTTGGTATGGGTGTAGCTGGATTGGA 120  
 QY 121 CAGCCTTCAGGAAGAGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAGCGC 180  
 Db 121 CAGCCTTCAGGAAGAGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAGCGC 180  
 QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATTCGAAGGATACCTTCCAGCAACAGGTA 240  
 Db 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATTCGAAGGATACCTTCCAGCAACAGGTA 240  
 QY 241 TTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGACATCTACTGTCTGGAAG 300  
 Db 241 TTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGACATCTACTGTCTGGAAG 300  
 QY 301 GTCTCTCTAACTGGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 360  
 Db 301 ATGGAT---GATTACGACGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 357  
 QY 361 TC 362  
 Db 358 TC 359  
 RESULT 13  
 AAT09299  
 ID AAT09299 standard; DNA; 417 BP.  
 XX  
 AC AAT09299;  
 XX  
 DT 25-JUL-1996 (first entry)  
 XX  
 DE Murine anti-Protein C Mab HPC-4 VH gamma coding region.  
 XX  
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
 KW zymogen; cleavage; mouse; humanised antibody; variable region;  
 KW light chain; inhibition; anticoagulant; coagulation; tumour; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FN W09534652-A1.  
 XX  
 PD 21-DEC-1995.  
 XX  
 PF 09-JUN-1995; 95WO-US07372.  
 XX  
 PR 10-JUN-1994; 94US-0259321.  
 XX  
 PA (OKLA-) OKLAHOMA MED RES FOUND.  
 XX  
 PI Esmon CT, Rezaie A;  
 XX  
 DR WPI; 1996-049681/05.  
 XX  
 DR P-PSDB; AAR88109.  
 XX  
 FT Calcium-binding monoclonal antibody immunoreactive with Protein C -  
 FT inhibits Protein C anticoagulant activation by  
 FT thrombin-thrombomodulin, e.g. for treating tumours  
 XX  
 PS Claim 4; Page 30; 41pp; English.  
 XX  
 CC This is the nucleotide sequence encoding the mature protein from the

PD 21-DEC-1995.  
 XX  
 XX 09-JUN-1995; 95WO-US07372.  
 XX  
 XX 10-JUN-1994; 94US-0259321.  
 XX  
 XX (OKLA-) OKLAHOMA MED RES FOUND.  
 XX  
 XX Esmon CT, Rezaie A;  
 XX  
 XX WPI; 1996-049681/05.  
 DR P-PSDB; AAR88107.  
 XX  
 XX Calcium-binding monoclonal antibody immunoreactive with Protein C -  
 PT inhibits Protein C anticoagulant activation by  
 PT thrombin-thrombomodulin, e.g. for treating tumours  
 XX  
 PS Claim 4; Page 29-30; 41pp; English.  
 XX  
 CC This is the nucleotide sequence encoding the heavy chain variable region  
 CC from the murine anti-protein C monoclonal antibody HPC-4 which  
 CC recognises the activation peptide region (AAR88106) of the heavy chain of  
 CC protein C, a vitamin K-dependent plasma protein zymogen. Protein C is  
 CC converted to activated protein C (APC) by cleavage between the Arg-Leu  
 CC amino acid contained within the activation peptide sequence. HPC-4  
 CC prevents protein C activation to APC by binding to this region. The DNA  
 CC sequences encoding the variable regions of the heavy and light chains of  
 CC the antibody (AAR09299-302) were used to construct humanised antibodies  
 CC using the PCR primers AAR09303-9. The humanised antibodies are useful as  
 CC inhibitors of coagulation and can be used for the treatment of tumours by  
 CC inhibiting the anticoagulant activity of APC by preventing conversion of  
 CC protein C to APC.  
 XX  
 SQ Sequence 417 BP; 89 A; 108 C; 106 G; 114 T; 0 other;  
 Query Match 81.7%; Score 296.4; DB 17; Length 417;  
 Best Local Similarity 90.6%; Pred. No. 2.6e-81;  
 Matches 328; Conservative 0; Mismatches 31; Indels 3; Gaps 1;  
 QY 1 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60  
 DB 58 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 117  
 QY 61 ACTGTGTTCTTCTCGGGTTTTCAGTGAGCACTCTGTTATGGTGTGAGCTGGATTGCA 120  
 DB 118 ACTGTGTTCTTCTCGGGTTTTCAGTGAGCACTCTGTTATGGTGTGAGCTGGATTGCT 177  
 QY 121 CAGCCCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTTACTGGGATGATGACAGCGC 180  
 DB 178 CAGCCCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTTGGTGGATGATGACAGCGC 237  
 QY 181 TATAACCCATCCTCGAAGACCGGGTTTACATCTCAAGGATACCTCCAGCAACCAAGTGA 240  
 DB 238 TATAACCCATCCTCGAAGACCGGGTTTACATCTCAAGGATACCTCCAGCAACCAAGTGA 297  
 QY 241 TTCTCTAAGTATCAGTGTGGACACTCGAGATGACTGCCATACCTACTGTGTCGAAGG 300  
 DB 298 TTCTCTAAGTATCAGTGTGGACACTCGAGATGACTGCCATACCTACTGTGTCGAAGG 357  
 QY 301 GTCTCTTAAGTATGACTGTGAGTACTGGGGTCAAGGAACCTCAGTCAACCGTCTCC 360  
 DB 358 ATGGAT---GATTACGACGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAACCGTCTCC 414  
 QY 361 TC 362  
 DB 415 TC 416  
 RESULT 14  
 ID AAR075889  
 XX AAR075889 standard; cDNA; 418 BP.  
 AC AAR075889;  
 XX 25-MAR-2003 (updated)  
 DT 21-AUG-1995 (first entry)  
 XX  
 DE Mouse heavy chain variable region in plasmid pUC-SK2-Vh.  
 XX  
 XX Primer; PCR; amplif; kappa; light chain; variable region; mouse; human;  
 KW interleukin; antibody; hybridoma; CDR; framework; constant region;  
 XX heavy chain; disorder; antigenicity; ds.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..417  
 FT /\*tag= a  
 FT /product= mouse heavy chain variable region  
 FT sig\_peptide  
 FT /\*tag= b  
 FT mat\_peptide  
 FT /\*tag= c  
 XX  
 PN WO9428159-A1.  
 XX  
 XX 08-DEC-1994.  
 PD  
 XX 30-MAY-1994; 94WO-JP00859.  
 PF  
 XX 31-MAY-1993; 93JP-0129787.  
 PR  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA (CHUS ) CHUGAI PHARM CO LTD.  
 XX  
 PI Hirata Y, Sato K, Tsuchiya M;  
 XX  
 XX WPI; 1995-022828/03.  
 DR P-PSDB; AAR67655.  
 XX  
 XX Antibody against IL-6 - useful for the therapy and treatment of  
 PT IL-6 related disorders.  
 PS  
 XX Claim 10; Page 49; 82pp; Japanese.  
 CC  
 CC The sequence of the gene encoding the heavy chain variable region of  
 CC the mouse anti-human interleukin-6 (IL-6) antibody. The fragment was  
 CC amplified by primers (AAQ75876-87) from cDNA derived from mRNA from  
 CC mouse SK2 hybridoma cells. The fragment was cloned into plasmid pUC19  
 CC to produce plasmid pUC-SK2-Vh. The inserted fragment is used to  
 CC generate constructs (see AAQ75914-7) encoding fragments of an antibody to  
 CC the human IL-6 comprising (a) a light chain with (i) a variable region  
 CC containing 3 complementarity determining regions (CDR) (AAR77201-3)  
 CC inserted into several framework regions (FR) (AAR77204-7) and (ii) a human  
 CC light chain constant region and (b) a heavy chain with (i) a variable  
 CC region containing 3 CDR (AAR77212-4) inserted into an FR (AAR77215-8) and  
 CC (ii) a human light chain constant region. The FR of the light chain may  
 CC be mouse derived (AAQ75888) or from the human antibody RE1. The heavy  
 CC chain FR may also be mouse derived (AAQ75889) or from the human antibody  
 CC DAW. The antibodies can be used in the treatment of IL-6 related  
 CC disorders. The antibodies are useful as they have low antigenicity due to  
 CC the use of human derived sequences and low antigenicity mouse derived  
 CC sequences.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 418 BP; 96 A; 113 C; 99 G; 110 T; 0 other;  
 Query Match 80.2%; Score 291; DB 16; Length 418;  
 Best Local Similarity 89.5%; Pred. No. 1.2e-79;  
 Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;  
 QY 1 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60  
 DB 58 CAGGTACTCTGAAGAAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 117  
 QY 61 ACTGTGTTCTTCTCGGGTTTTCAGTGAGCACTCTGTTATGGTGTGAGCTGGATTGCA 120

Db 118 ACTTGTTCTTCTCTGGTTTTCACCTGAACACTTCTGGTATGACCGTAGGTGGATTCTG 177  
Qy 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTTGGATGATGACAAAGCG 180  
Db 178 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTGGTGAATGATGATAAGTAC 237  
Qy 181 TATACCCATCCCTGAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 240  
Db 238 TATACCCAGCCCTGAAAGCGCGGTCAATCTCCAAGGATACCTCCAAACAGGTA 297  
Qy 241 TTCTCTCAAGATCACCAGTGTGACACTCGAGATCTGCCACATACTACTGTCTCGAAG 300  
Db 298 TTCTCTCAAGATCACCAGTGTGCTCACTGAGATCTGCCACATACTACTGTCTCGAAG 357  
Qy 301 GTCTCTCAAGTCTGATGACTGACTGCTGGGTCAGGACCTCACTACCGTCTCC 360  
Db 358 GAGGAT---TAGCAGGAAGCTATGACTACTGGGTCAAGGAACCTCAGTACCGGTCTCC 414  
Qy 361 TCA 363  
Db 415 TCA 417

RESULT 15  
ID ABN84609  
XX ABN84609 standard; cDNA; 465 BP.  
AC ABN84609;  
XX  
DT 29-OCT-2002 (first entry)  
XX  
DE Anti-Streptococcus mutans surface antigen MAb SWLA2 VH coding region.  
XX  
KW Streptococcus mutans; monoclonal antibody; Mab; mouse;  
KW Chimeric antibody; antibody; anticaries; transgenic plant;  
KW transgenic animal; caries; immunotherapy; therapy; gene; ss.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT 13..441  
FT /\*tag= a  
FT /partial  
FT /product= "SWLA2 heavy chain variable region"  
FT /note= "the CDS does not include a stop codon"  
XX  
PN US2002068066-A1.  
XX  
PD 06-JUN-2002.  
XX  
PF 15-JUN-2001; 2001US-0881823.  
XX  
PR 20-AUG-1999; 99US-0378577.  
XX  
PA (SHIW/) SHI W.  
PA (MORR/) MORRISON S L.  
PA (TRIN/) TRINH K.  
PA (WIMS/) WIMS L.  
PA (CHEN/) CHEN L.  
PA (ANDE/) ANDERSON M H.  
XX  
PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;  
XX  
DR WPI; 2002-565838/60.  
DR P-PSDB; ABB79728.  
XX  
PT Treatment and prevention of dental caries in mammals, in particular  
PT humans by orally administering genetically engineered or purified  
PT antibodies that bind to surface antigens of cariogenic organisms -  
XX  
PS Claim 6; Fig 2B; 30pp; English.  
XX

CC The present sequence is the coding sequence of the heavy chain  
CC variable region (VH) of the murine monoclonal antibody SWLA2 (IGG),  
CC which binds specifically to the surface antigens of cariogenic type  
CC c Streptococcus mutans (ATCC 25175). The coding sequence was  
CC obtained from SWLA2 (ATCC HB 12560) hybridoma cells by PCR  
CC amplification (see also ABN84625 and ABN84622). The SWLA2 VH and  
CC VL (see ABN84608) coding sequences were used in the preparation of  
CC chimeric monoclonal antibody TFE comprising SWLA2 variable regions  
CC and human antibody constant regions. Such chimeric monoclonal  
CC antibodies can be used to prevent or treat dental caries in humans.  
CC The antibodies engage the effector apparatus of the human immune  
CC system when they bind cariogenic organisms, resulting in their  
CC destruction. The antibodies may be produced in edible plants,  
CC in transgenic animals, or in chicken eggs for oral ingestion.  
XX  
SQ Sequence 465 BP; 108 A; 124 C; 113 G; 120 T; 0 other;  
  
Query Match 78.3%; Score 284.4; DB 24; Length 465;  
Best Local Similarity 88.0%; Pred. No. 1.4e-77;  
Matches 322; Conservative 0; Mismatches 41; Indels 3; Gaps 1;  
  
Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60  
Db 70 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 129  
Qy 61 ACTTGTCTTTCTCTCGGTTTTCATGAGCAGCTTCTGGTATGGGTGAGCTGGATTGCA 120  
Db 130 ACTTGTCTTTCTCTCGGTTTTCATGAGCAGCTTCTGGTATGGGTGAGCTGGATTGCT 189  
Qy 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAGCG 180  
Db 190 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGGACACATTTGGTGAATGATATAGTAC 249  
Qy 181 TATAACCCATCCCTGAAAGAGCGGCTTACAATCTCCAAGGATACCTCCAGCAACAGGTA 240  
Db 250 TATAACACAGTCTCTGAAGAGCGGCTCACAATCTCCAAGGATACCTCCAAACAGGTA 309  
Qy 241 TTCTCTCAAGATCACCAGTGTGAGACACTCGAGATACTGCCACATACTACTGTCTCGAAG 300  
Db 310 TTCTCTCAAGATCACCAGTGTGAGACACTCGAGATACTGCCACATACTACTGTCTCGAAG 369  
Qy 301 GTCTCTCTAACTGCCT---ATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAACGTC 357  
Db 370 GAGGGGGGCTCGGGCTACGATGTTATGGACTACTGGGGTCAAGGAATCTCAGTCAACGTC 429  
Qy 358 TCCTCA 363  
Db 430 TCCTCA 435

Search completed: January 14, 2004, 16:03:11  
Job time : 189.476 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 15:52:50 ; Search time 1460.9 Seconds  
(without alignments)  
6039.083 Million cell updates/sec

Title: US-09-759-112a-5

Perfect score: 363

Sequence: 1 caggttactctgaagagtc.....cctcagtcaccgtctctctca 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em\_eetba:\*

2: em\_eethum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_man:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vri:\*

28: gb\_gssl:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	322.8	88.9	451	14	CAS80198 K0748C01-
2	322.8	88.9	485	14	CAS78844 K0729C06-
3	302.6	83.4	864	10	BE309336 601093720
4	300.6	82.8	913	10	BF593109 602098016

5	298.6	82.3	666	12	BG963642
6	295.8	81.5	940	10	BF178694
7	292.6	80.6	947	13	BQ943210
8	281.4	77.5	652	12	BQ943210
9	278	76.6	391	10	AW989547
10	271.8	74.9	485	14	CAS79006
11	271.8	74.9	485	14	CAS79140
12	271.6	74.8	920	13	BQ231128
13	267.6	73.7	379	10	BQ231128
14	265.8	73.2	428	14	CAS78658
15	262.6	72.3	363	10	BQ70162
16	262.4	72.3	366	10	BQ70162
17	260.6	71.8	438	9	AA80491
18	259.8	71.6	900	10	BF581194
19	259.6	71.5	377	10	BQ73796
20	259.6	71.5	589	28	AZ882936
21	254.2	70.0	920	10	BF580719
22	253.4	69.8	670	10	BE289865
23	243.6	67.1	374	10	BQ88022
24	237	65.3	769	10	BF582574
25	234.8	64.7	340	10	BQ869851
26	224	61.7	330	10	BQ870527
27	209.8	57.8	327	13	BY346637
28	207.8	57.2	827	12	BM007964
29	206.2	56.8	904	10	EG758540
30	200.6	55.3	311	9	AI466485
31	196.6	54.2	941	13	BQ707283
32	196.6	54.2	945	13	BQ708104
33	195	53.7	1083	12	BI762661
34	192	52.9	1030	13	EX337695
35	191.8	52.8	384	10	BE246586
36	191.8	52.8	385	10	BE247351
37	191.8	52.8	562	14	CB555600
38	191.8	52.8	1167	13	EX381021
39	191.6	52.8	923	10	BF663900
40	190.2	52.4	439	10	BE247437
41	189	52.1	955	13	BQ711772
42	189	52.1	956	13	BQ709744
43	188.2	51.8	831	10	BF238095
44	186.8	51.5	324	10	BQ872886
45	186.8	51.5	620	12	BM788928

## ALIGNMENTS

RESULT 1	CAS80198	451 bp	linear	EST 19-NOV-2002
CAS80198	K0748C01-EN NIA Mouse Hematopoietic Stem Cell	cdna library (Long)	Mus musculus	cdna clone NIA:K0748C01
LOCUS	IMAGE:30078168 5', mRNA sequence.			
DEFINITION	CAS80198			
ACCESSION	CAS80198			
VERSION	CAS80198.1	GI:25128589		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
TITLE	1 (bases 1 to 451)			
JOURNAL	Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,			
COMMENT	Aiba, K., Taub, D., Longo, D.L., Keller, J. and K.M.S.H.			
	Systematic Analyses of NIA Mouse Hematopoietic Stem Cell			
	(Lin-/c-Kit-/Sca-1-) cdna Library (Long)			
	Unpublished			
	Other ESTs: K0748C01-3			
	Contact: Dawood B. Dudekula			
	Laboratory of Genetics			
	National Institute on Aging/National Institutes of Health			
	333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA			
	Email: cdna@gsun.grc.nia.nih.gov			
	Plate: K0748 row: C column: 01			
	Seq primer: M13 Reverse			



High quality sequence stop: 451

```

POLYA-No. Location/Qualifiers
1. .451
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6Ncr"
/db_xref="niaEST:K0748C01-5N"
/db_xref="taxon:10090"
/clone="NIA:K0748C01 IMAGE:30078168"
/tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)"
/dev stage="Age approx.10 weeks old"
/lab_host="DH10B"
/clone_lib="NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Drs. Dennis Taub, Dan Longo (National Cancer Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-PGACTAGTCTAGATCGAGCGCCGCTTTT-3'] from 0.9 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LI-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."
```

BASE COUNT 99 a 129 c 104 g 119 t

ORIGIN

```

Query Match 88.9%; Score 322.8; DB 14; Length 451;
Best Local Similarity 94.5%; Pred. No. 6e-84;
Matches 346; Conservative 0; Mismatches 17; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGAGCCCTCCAGACCCCTCAGTCTG 60
DB 38 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGTCTCCAGACCCCTCAGTCTG 97
QY 61 ACTTGTTCTTCTCTGGTTTCTACTGAGCACTCTCGTATGGTGTGAGCTGGATTGGA 120
DB 98 ACTTGTTCTTCTCTGGTTTCTACTGAGCACTCTCGTATGGTGTGAGCTGGATTGGA 157
QY 121 CAGCCTTCAGAAAGGCTCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCGC 180
DB 158 CAGCCTTCAGAAAGGCTCTGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCGC 217
QY 181 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAAAGATACCTCCAGCAACCGAGTA 240
DB 218 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAAAGATACCTCCAGCAACCGAGTA 277
QY 241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTCCACATACACTGTGTGTC---GA 297
DB 278 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTCCACATACACTGTGTGTCGAGA 337
QY 298 AGGCTCTCTTAAGTGGCTATGCTATGAGTACTGCGGTCAAGGAACCTCAGTCACCGTC 357
DB 338 AGTGAATACCTCCATATGCTATGCTATGCTATGCGGTCAAGGAACCTCAGTCACCGTC 397
QY 358 TCCTCA 363
|||||

```

398 TCCTCA 403

Db

RESULT 2

CA578844

LOCUS

DEFINITION

K0729C06-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long) Mus musculus cDNA clone NIA:K0729C06 IMAGE:30076349 5', mRNA sequence.

ACCSSION

CA578844

VERSION

CA578844.1 GI:25127235

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 485)

Alba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H., Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long) Unpublished

JOURNAL

Other ESTs: K0729C06-3

COMMENT

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

Plate: K0729 row: C column: 06

Seq primer: M13 Reverse

High quality sequence stop: 485

POLYA-No.

Location/Qualifiers

1. .485

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6Ncr"

/db\_xref="niaEST:K0729C06-5N"

/db\_xref="taxon:10090"

/clone="NIA:K0729C06 IMAGE:30076349"

/tissue\_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)"

/dev stage="Age approx.10 weeks old"

/lab\_host="DH10B"

/clone\_lib="NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"

/note="Vector: pSPORT1 (Invitrogen); Site\_1: SalI; Site\_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Drs. Dennis Taub, Dan Longo (National Cancer Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-PGACTAGTCTAGATCGAGCGCCGCTTTT-3'] from 0.9 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LI-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 105 a 138 c 114 g 128 t

ORIGIN

Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH					
BASE COUNT	171 a	260 c	222 g	211 t	
ORIGIN					
Query Match	83.4%; Score 302.6; DB 10; Length 864;				
Best Local Similarity	92.2%; Pred. No. 6.6e-78;				
Matches 346; Conservative	0; Mismatches 19; Indels 10; Gaps 2;				
QY	1	CAGGTTACTCTGAAGAAGTCTGGCCCTCGGATATTGCAGCCCTCCAGACCCCTCAGTCGTG	60		
DB	38	CAGGTTACTCTGAAGAAGTCTGGCCCTCGGATATTGCAGCCCTCCAGACCCCTCAGTCGTG	97		
QY	61	ACTTGTTCTTCTCTGGGTTTTCACTGAGCACTTCTTGTAATGGGTGTGAGCTGGATCGA	120		
DB	98	ACTTGTTCTTCTCTGGGTTTTCACTGAGCACTTCTTGTAATGGGTGTGAGCTGGATCGT	157		
QY	121	CAGCCTTCAGAAAGGGTCTGGGTGGCTGGCACACATTTACTGGGATGTACAAGCGC	180		
DB	158	CAGCCTTCAGAAAGGGTCTGGGTGGCTGGCACACATTTACTGGGATGTACAAGCGC	217		
QY	181	TATAACCCTCCCTGAAGAGCGGCTTACAATCTCCAAGTATCCTCCAGCAACCAAGGTA	240		
DB	218	TATAACCCTCCCTGAAGAGCGGCTTACAATCTCCAAGTATCCTCCAGCAACCAAGGTA	277		
QY	241	TTCCCTCAGATCACCAGTGTGGACACTCGATATCTGCCATCTACTCTGTCTC---GA	297		
DB	278	TTCCCTCAGATCACCAGTGTGGACACTCGATATCTGCCATCTACTCTGTCTCGAAGA	337		
QY	298	AGGGTCTCTTAACCTGCTATGCTATGACTACTGGGCTCAAGGAACCTCAGTCACCGTC	357		
DB	338	AGTGATTACCTCCATCATCTATGCTATGACTACTGGGCTCAAGGAACCTCAGTCACCGTC	397		
QY	358	TCCTCA 363			
DB	398	TCCTCA 403			
RESULT 3					
BE309336					
LOCUS	601093720F1 NCI_CGAP_Mam5 Mus musculus cdna clone IMAGE:3488309 5',				
DEFINITION	mRNA sequence.				
ACCESSION	BE309336				
VERSION	1 GI:9167366				
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cdna Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM8527 row: h column: 06 High quality sequence stop: 645.				
FEATURES	Location/Qualifiers				
source	1..864				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/strain="C57BL/6J"				
	/db_xref="taxon:10090"				
	/clone="IMAGE:3488309"				
	/tissue_type="tumor, gross tissue"				
	/dev_stage="7 months"				
	/lab_host="DH10B"				
	/clone_lib="NCI CGAP Mam5"				
	/note="Organ: mammary; Vector: pCMV-Sport6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT."				
Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH					
BASE COUNT	171 a	260 c	222 g	211 t	
ORIGIN					
Query Match	83.4%; Score 302.6; DB 10; Length 864;				
Best Local Similarity	92.2%; Pred. No. 6.6e-78;				
Matches 344; Conservative	0; Mismatches 19; Indels 10; Gaps 2;				
QY	1	CAGGTTACTCTGAAGAAGTCTGGCCCTCGGATATTGCAGCCCTCCAGACCCCTCAGTCGTG	60		
DB	43	CAGGTTACTCTGAAGAAGTCTGGCCCTCGGATATTGCAGCCCTCCAGACCCCTCAGTCGTG	102		
QY	61	ACTTGTTCTTCTCTGGGTTTTCACTGAGCACTTCTTGTAATGGGTGTGAGCTGGATCG	119		
DB	103	ACTTGTTCTTCTCTGGGTTTTCACTGAGCACTTCTTGTAATGGGTGTGAGCTGGATCG	162		
QY	120	ACAGCCTTCAGAAAGGGTCTGGGATGGCTGGCACACATTTACTGGGATGTACAAGCGC	179		
DB	163	TCAGCCTTCAGAAAGGGTCTGGGATGGCTGGCACACATTTACTGGGATGTACAAGCGC	222		
QY	180	CTATAACCCATCCCTGAAGAGCCCGCTTACAATCTCCAAGGATACCTCCAGAACCCAGGT	239		
DB	223	CTATAACCCATCCCTGAAGAGCCCGCTTACAATCTCCAAGGATACCTCCAGAACCCAGGT	282		
QY	240	ATTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATCTACTCTGTCTCGAAG	299		
DB	283	ATTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATCTACTCTGTCTCGAAT	342		
QY	300	GCTCTCTCTAACTG-----CCTATGCTATGACTACTCTGGGGTCAAGGAACCTCAGT	350		
DB	343	TTATTACCAGGTGTGATGCTTACTATGCTATGACTACTCTGGGGTCAAGGAACCTCAGT	402		
QY	351	CACCGTCTCTCTCA 363			
DB	403	CACCGTCTCTCTCA 415			
RESULT 4					
BE583109					
LOCUS	602098016F1 NCI_CGAP_Co24 Mus musculus cdna clone IMAGE:4218099 5',				
DEFINITION	mRNA sequence.				
ACCESSION	BF583109				
VERSION	BF583109.1 GI:11656827				
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9797 row: p column: 04 High quality sequence stop: 656.				
FEATURES	Location/Qualifiers				
source	1..913				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/strain="FVB/N"				
	/db_xref="taxon:10090"				
	/clone="IMAGE:4218099"				

```
/lab_host="PH108 (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      183 a   261 c   250 g   219 t
ORIGIN

Query Match      82.8%; Score 300.6; DB 10; Length 913;
Best Local Similarity 90.5%; Pred. No. 2.6e-77;
Matches 334; Conservative 0; Mismatches 29; Indels 6; Gaps 1;

QY 1 CAGGTTACTCTGAAGAGCTGSCCTGGATATTGACGCTCCAGACCCCTCAGTCTG 60
DB 60 CAGGTTACTCTGAAGAGCTGSCCTGGATATTGACGCTCCAGACCCCTCAGTCTG 119
QY 61 ACTTGTCTTTCTCTGGTTTCACTGACACCTTCTGGTATGGGTGAGCTGGATTG 120
DB 120 ACTTGTCTTTCTCTGGTTTCACTGACACCTTCTGGTATGGGTGAGTGGATTG 179
QY 121 CAGCCTTCAGGAAGGCTCGAGTGGCTGGACACATTTACTGGGATGATCACAAGCG 180
DB 180 CAGCCTTCAGGAAGGCTCGAGTGGCTGGACACATTTACTGGGATGATCACAAGCG 239
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 240
DB 240 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 299
QY 241 TTCTCAAGATCACCAGTGGACCTCGAGATCTGCCACATCTACTGTCTGCTCG --- 296
DB 300 TTCTCAAGATCACCAGTGGACCTCGAGATCTGCCACATCTACTGTCTGCTCG 359
QY 297 --AAGGCTCTCTCTAACTGCTATGTGACTGCTGGGCTCAAGAAACCTCAGTCA 354
DB 360 TATGATGTTTACGCATATTACTATGCTCTGGACTCTGGGCTCAAGAAACCTCAGTCA 419
QY 355 GTCTCTCTCA 363
DB 420 GTCTCTCTCA 428

RESULT 5
BG963642
LOCUS      602828443F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983155 5',
DEFINITION mRNA sequence.
ACCESSION BG963642
VERSION    BG963642.1 GI:14351279
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 666)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/
TITLES    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapsb-remail.nih.gov
          Tissue Procurement: Jeffrey E. Green, M.D.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM10987 row: e column: 12
          High quality sequence stop: 658.
          Location/Qualifiers
            1..666
              /organism="Mus musculus"
              /mol_type="mRNA"
```

```
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Co24"
/clone_host="PH108 (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      157 a   186 c   159 g   164 t
ORIGIN

Query Match      82.3%; Score 298.6; DB 12; Length 666;
Best Local Similarity 91.5%; Pred. No. 9e-77;
Matches 343; Conservative 0; Mismatches 19; Indels 13; Gaps 2;

QY 1 CAGGTTACTCTGAAGAGCTGSCCTGGATATTGACGCTCCAGACCCCTCAGTCTG 60
DB 59 CAGGTTACTCTGAAGAGCTGSCCTGGATATTGACGCTCCAGACCCCTCAGTCTG 117
QY 61 ACTTGTCTTTCTCTGGTTTCACTGACACCTTCTGGTATGGGTGAGCTGGATTG 120
DB 118 ACTTGTCTTTCTCTGGTTTCACTGACACCTTCTGGTATGGGTGAGCTGGATTG 177
QY 121 CAGCCTTCAGGAAGGCTCGAGTGGCTGGACACATTTACTGGGATGATCACAAGCG 180
DB 178 CAGCCTTCAGGAAGGCTCGAGTGGCTGGACACATTTACTGGGATGATCACAAGCG 237
QY 181 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 240
DB 238 TATAACCCATCCCTGAAGAGCGGCTTACAATCTCCAGGATACCTCCAGCAACAGGTA 297
QY 241 TTCTCAAGATCACCAGTGGACCTCGAGATCTGCCACATCTACTGTCTGCTG --- 296
DB 298 TTCTCAAGATCACCAGTGGACCTCGAGATCTGCCACATCTACTGTCTGCTG 357
QY 297 -----AAGGCTCTCTCTAACTGCTATGTGACTGCTGGGCTCAAGAAACCTCA 348
DB 358 TATAGTTACTATAGTTAGGAATATTACTATGCTATGGAATCTGGGCTCAAGAAACCTCA 417
QY 349 GTCAACCGCTCTCTCA 363
DB 418 GTCAACCGCTCTCTCA 432

RESULT 6
BF178694
LOCUS      601806679F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4037587 5',
DEFINITION mRNA sequence.
ACCESSION BF178694
VERSION    BF178694.1 GI:11056836
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 940)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/
TITLES    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapsb-remail.nih.gov
          Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM9314 row: n column: 20
          High quality sequence stop: 631.
          Location/Qualifiers
```

```

source
1. .940
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4037597"
/dev_stage="7 months"
/lab_host="DHI0B"
/clone_lib="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
BASE COUNT 206 a 267 c 259 g 207 t 1 others
ORIGIN
Query Match 81.5%; Score 295.8; DB 10; Length 940;
Best Local Similarity 89.7%; Pred. No. 6.8e-76;
Matches 331; Conservative 0; Mismatches 32; Indels 6; Gaps 1;
QY 1 CAGGTTACTCTGAAGAAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
DB 58 CAGGTTACTCTGAAGAAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 117
QY 61 ACTGTCTTTCTCTGGTTTTCACTGAGCACTTCTGGTATGGTGTGAGTGGATTGCA 120
DB 118 ACTGTCTTTCTCTGGTTTTCACTGAGCACTTCTGGTATGGTGTGAGTGGATTGCA 177
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCGC 180
DB 178 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCAGACATTTACTGGGATGACAAATAGTAC 237
QY 181 TATAACCCATCCCTGGAAGAGCCGGCTTACAACTCCAAAGGATACCTCCAGCAACCAAGGTA 240
DB 238 TTTAAACCCATCCCTGGAAGAGCCGGCTTACAACTCCAAAGGATACCTCCAGCAACCAAGGTA 297
QY 241 TTCTCTAAGATCACCAGTGTGGACCTGAGATGACTGCGACATCTACTGTGTGTCGAAGG 300
DB 298 TTCTCTAAGATCACCAGTGTGGACCTGAGATGACTGCGACATCTACTGTGTGTCGAAGG 357
QY 301 GTCTCTTAAGTCTG-----CTATGCTATGAGTCTACTGGGGTCAAGGAACCTCAGTCAAC 354
DB 358 CGGTTACTAGTCTCTTTACTATGCTTTGAGTCTACTGGGGTCAAGGAACCTCAGTCAAC 417
QY 355 GTCTCTCA 363
DB 418 GTCTCTCA 426

RESULT 7
BQ943210 947 bp mRNA linear EST 21-AUG-2002
LOCUS
DEFINITION
AGENCOURT.8836910 NCI CGAP Co24 Mus musculus cDNA clone
IMAGE:6398059 5', mRNA sequence.
ACCESSION
BQ943210
VERSION
BQ943210.1 GI:22358688
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 947)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM13896 row: o column: 20
High quality sequence stop: 669.
Location/Qualifiers
1. .947
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6398059"
/lab_host="DHI0B (T1 phage-resistant)"
/clone_lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP library."
BASE COUNT 218 a 272 c 235 g 221 t 1 others
ORIGIN
Query Match 80.6%; Score 292.6; DB 13; Length 947;
Best Local Similarity 87.9%; Pred. No. 5.9e-75;
Matches 319; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1 CAGGTTACTCTGAAGAAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60
DB 72 CAGGTTACTCTGAAGAAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 131
QY 61 ACTGTCTTTCTCTGGTTTTCACTGAGCACTTCTGGTATGGTGTGAGTGGATTGCA 120
DB 132 ACTGTCTTTCTCTGGTTTTCACTGAGCACTTCTGGTATGGTGTGAGTGGATTGCA 191
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCGC 180
DB 192 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCAGACATTTACTGGGATGATGACAGCGC 251
QY 181 TATAACCCATCCCTGGAAGAGCCGGCTTACAACTCCAAAGGATACCTCCAGCAACCAAGGTA 240
DB 252 TATAACCCAGCCCTGGAAGAGCCGGCTGACAACTCTCCAAGGATACCTCCAGCAACCAAGGTA 311
QY 241 TTCTCTAAGATCACCAGTGTGGACCTCGAGATACCTGCCACATCTACTGTGTGCAAGG 300
DB 312 TTCTCTAAGATCACCAGTGTGGACCTCGAGATACCTGCCACATCTACTGTGTGCAAGGTA 371
QY 301 GTCTCTTAAGTCTGCTATGCTATGAGTCTACTGGGGTCAAGGAACCTCAGTCAACCGTCTCC 360
DB 372 AGGATAGTAACTACTGTGTTCTGATGTTCTGGGGCGCAGGACCGGTCAACCGTCTCC 431
QY 361 TCA 363
DB 432 TCA 434

RESULT 8
BQ963304 652 bp mRNA linear EST 12-JUN-2001
LOCUS
DEFINITION
602827722F1 NCI CGAP Co24 Mus musculus cDNA clone IMAGE:4982549 5',
mRNA sequence.
ACCESSION
BQ963304
VERSION
BQ963304.1 GI:14350941
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 652)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

```

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LAM10985 row: 1 column: 06  
High quality sequence stop: 648.  
Location/Qualifiers

FEATURES  
source  
1. .652  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4982549"  
/lab\_host="DH10B (Tl phage-resistant)"  
/clone\_lib="NCI CGAP Co24"  
/note="Organ: colon; Vector: pCMV-Sport6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 Kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."  
BASE COUNT 141 a 184 c 163 g 164 t  
ORIGIN

Query Match 77.5%; Score 281.4; DB 12; Length 652;  
Best Local Similarity 86.0%; Pred. No. 1e-71;  
Matches 312; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 CAGTTTACTCTGAAGAGTCTGGCCCTGGATATTCAGCCCTCCAGACCTCCAGTCTG 60  
DB 53 CAGTTTACTCTGAAGAGTCTGGCCCTGGATATTCAGCCCTCCAGACCTCCAGTCTG 112  
QY 61 ACTTGTCTTTCTCTGGTTTCACTGAGCATTCTGGTATGGTGTGAGCTGGATTGGA 120  
DB 113 ACTTGTCTTTCTCTGGTTTCACTGAGCATTCTGGTATGGTGTGAGCTGGATTGGA 172  
QY 121 CAGCCTTCAGGAAGGCTCTGGATGGCTGGACACATTTACTGGATGATGACAGCGC 180  
DB 173 CAGCCTTCAGGAAGGCTCTGGATGGCTGGACACATTTACTGGATGATGACAGCGC 232  
QY 181 TATAATCCATCCCTGAAGAGCCGGCTTACAACTCCAAAGGATACCTCCAGCAACAGGTA 240  
DB 233 TATAATCCATCCCTGAAGAGCCGGCTTACAACTCCAAAGGATACCTCCAGCAACAGGTA 292  
QY 241 TTCTCTAAGATCACCAGTGTGGACCTCGAGATCTGCCACATCTACTGTGCTGAGG 300  
DB 293 TTCTCTAAGATCACCAGTGTGGACCTCGAGATCTGCCACATCTACTGTGCTGAGG 352  
QY 301 GTCTCTTAATCTGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAACGCTCC 360  
DB 353 CCTTATTTTCCCTATTGGTACTTCGATGCTGGGGTCAAGGAACCTCAGTCAACGCTCC 412  
QY 361 TCA 363  
DB 413 TCA 415

RESULT 9  
LOCUS AW989547 391 bp mRNA linear EST 02-JUN-2000  
DEFINITION ug14h06.y1 Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:1531643 5' similar to SW:EV2H HUMAN P04438 IG HEAVY CHAIN V-II REGION SENS PRECURSOR. [1] ;, mRNA sequence.  
ACCESSION AW989547  
VERSION AW989547.1 GI:8184975  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 391)  
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), TITLE

Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cygabs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:947743  
Trace considered overall poor quality  
Seq primer: -40RP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source  
1. .391  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1531643"  
/sex="female (lactating)"  
/tissue\_type="mammary gland"  
/lab\_host="DH10B"  
/clone\_lib="Soares mammary gland NMLMG"  
/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 88 a 107 c 90 g 106 t  
ORIGIN

Query Match 76.6%; Score 278; DB 10; Length 391;  
Best Local Similarity 95.0%; Pred. No. 8.2e-71;  
Matches 287; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 CAGTTTACTCTGAAGAGTCTGGCCCTGGATATTCAGCCCTCCAGACCTCCAGTCTG 60  
DB 56 CAGTTTACTCTGAAGAGTCTGGCCCTGGATATTCAGCTCTCCAGACCTCCAGTCTG 115  
QY 61 ACTTGTCTTTCTCTGGTTTCACTGAGCATTCTGGTATGGTGTGAGCTGGATTGGA 120  
DB 116 ACTTGTCTTTCTCTGGTTTCACTGAGCATTCTGGTATGGTGTGAGCTGGATTGGA 175  
QY 121 CAGCCTTCAGGAAGGCTCTGGATGGCTGGACACATTTACTGGATGATGACAGCGC 180  
DB 176 TAGCCTTCACGAAGGCTCTGGATGGCTGGACACATTTACTGGATGATGACAGCTT 235  
QY 181 TATAATCCATCCCTGAAGAGCCGGCTTACAACTCCAAAGGATACCTCCAGCAACAGGTA 240  
DB 236 TATAATCCATCCCTGAAGAGCCGGCTTACAACTCCAAAGGATACCTCCAGCAACAGGTA 295  
QY 241 TTCTCTAAGATCACCAGTGTGGACCTCGAGATCTGCCACATCTACTGTGCTGGAAG 300  
DB 296 TTCTCTAAGATCACCAGTGTGGACCTCGAGATCTGCCACATCTACTGTGCTGGAAG 355  
QY 301 GT 302  
DB 356 GT 357

RESULT 10  
LOCUS CA579006 485 bp mRNA linear EST 19-NOV-2002  
DEFINITION K0731E07-SN NIA Mouse Hematopoietic Stem Cell (Lin-/c-kit-/Sca-1-) cDNA Library (Long) Mus musculus cDNA clone NIA:K0731E07 IMAGE:30076566 5' ;, mRNA sequence.  
ACCESSION CA579006  
VERSION CA579006.1 GI:25127397  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 485)  
 AUTHORS Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G.,  
 Alba,K., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.  
 TITLE Systematic Analyses of NIA Mouse Hematopoietic Stem Cell  
 JOURNAL (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)  
 COMMENT Unpublished  
 Other ESTs: K0731E07-3  
 Contact: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@lgsun.grc.nia.nih.gov  
 Plate: K0731 row: E column: 07  
 Seq primer: M13 Reverse  
 High quality sequence stop: 485  
 POLYA=No.

FEATURES  
 source  
 1..485  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6Ncr"  
 /db\_xref="niaEST:K0731E07-5N"  
 /db\_xref="taxon:10090"  
 /clone="NIA:K0731E07 IMAGE:30076566"  
 /tissue\_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)"  
 /dev\_stage="Age approx.10 weeks old"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse Hematopoietic Stem Cell  
 (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"  
 /notes="Vector: pSPORT1 (Invitrogen); Site\_1: SalI; Site\_2:  
 NotI; Mouse cDNA project by the Laboratory of Genetics,  
 National Institute on Aging (NIA), Intramural Research  
 Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is  
 a long-transcript enriched cDNA library (Ref. Genome Res.  
 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were  
 obtained from Drs. Dennis Taub, Dan Longo (National  
 Institute on Aging, USA), Jonathan Keller (National Cancer  
 Institute, USA). Double-stranded cDNAs were synthesized  
 with an oligo(dT) primer [Invitrogen]:  
 5'-pGATCTACTGATCGAGCGCGCCCTCTTTT-3' from  
 0.9 ug of total RNA, treated with T4 DNA polymerase, and  
 purified by ethanol-precipitation. The cDNAs were ligated  
 to Lona-linker IL-Sal4, purified by phenol/chloroform, and  
 separated from free linkers by Centricon 100. Then, the  
 cDNAs were amplified by long-range high fidelity PCR using  
 Ex Taq polymerase (Takara) with a primer Sal4-S. The  
 products were purified by phenol/chloroform and Centricon  
 100. The cDNAs were digested with SalI and NotI enzymes  
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
 The DH10B E. coli host was transformed with the ligation  
 mixture by the standard chemical method. The average  
 insert size is about 2.1 kb. The library was constructed  
 by Yulan Piao (NIA)."

BASE COUNT 101 a 136 c 119 g 129 t

ORIGIN  
 Query Match 74.9% Score 271.8; DB 14; Length 485;  
 Best Local Similarity 85.68; Pred No. 5.9e-69;  
 Matches 316; Conservative 0; Mismatches 47; Indels 6; Gaps 1;  
 1 CAGTTACTGAAAGAGTCTGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
 35 CAGGTTACTGAAAGAGTCTGCCCTGGTATATTCAGCCCTCCAGACCCCTCAGTCTG 94  
 61 ACTTGTCTTCTCTGGTCTTTCACATGAGCACTCTGGTATGGTGTGAGCTGGATCGA 120  
 95 ACTTGTTCTTCTCTGGTCTTTCACATGAGCACTCTGGTATGGTGTGAGCTGGATCGT 154  
 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCCACACATTCTGGGATGATGACAGCCGC 180  
 155 CAGCCTTCAGGAAGGATCTGGAGTGGCTGGCCACACATTCTGGGATGATGACAGCAC 214

QY 181 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGSTA 240  
 DB 215 TATAACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGSTA 274  
 QY 241 TTCTCTAAGATCACCAAGTGTGGACACTCGAGATCTCCACATCTACTCTGCTCGAAGG 300  
 DB 275 TTCTCTAAGATCACCAAGTGTGGACACTCGAGATCTCCACATCTACTCTGCTCGGCTG 334  
 QY 301 CTCTCTCTAACTG-----CCTATGCTTGGACTACTTGGGGTCAAGAACTCAGTCACC 354  
 DB 335 GCCATTATGACGGGGGATCTGGTACTTTCATGCTCTGGGGCACAGGACCCAGTCACC 394  
 QY 355 GTCTCTCTCA 363  
 DB 395 GTCTCTCTCA 403

RESULT 11  
 CA579140  
 LOCUS  
 DEFINITION K0733C10-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long) Mus musculus cDNA clone NIA:K0733C10 IMAGE:30076737 5', mRNA sequence.  
 ACCESSION CA579140  
 VERSION CA579140.1 GI:25127531  
 KEYWORDS EST.  
 ORGANISM Mus musculus (house mouse)  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 485)  
 AUTHORS Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G., Alba,K., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.  
 TITLE Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)  
 JOURNAL Unpublished  
 COMMENT Other ESTs: K0733C10-3  
 Contact: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@lgsun.grc.nia.nih.gov  
 Plate: K0733 row: C column: 10  
 Seq primer: M13 Reverse  
 High quality sequence stop: 485  
 POLYA=No.

FEATURES  
 source  
 1..485  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6Ncr"  
 /db\_xref="niaEST:K0733C10-5N"  
 /db\_xref="taxon:10090"  
 /clone="NIA:K0733C10 IMAGE:30076737"  
 /tissue\_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)"  
 /dev\_stage="Age approx.10 weeks old"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse Hematopoietic Stem Cell  
 (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"  
 /notes="Vector: pSPORT1 (Invitrogen); Site\_1: SalI; Site\_2:  
 NotI; Mouse cDNA project by the Laboratory of Genetics,  
 National Institute on Aging (NIA), Intramural Research  
 Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is  
 a long-transcript enriched cDNA library (Ref. Genome Res.  
 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were  
 obtained from Drs. Dennis Taub, Dan Longo (National  
 Institute on Aging, USA), Jonathan Keller (National Cancer  
 Institute, USA). Double-stranded cDNAs were synthesized  
 with an oligo(dT) primer [Invitrogen]:  
 5'-pGATCTACTGATCGAGCGCGCCCTCTTTT-3' from  
 0.9 ug of total RNA, treated with T4 DNA polymerase, and  
 purified by ethanol-precipitation. The cDNAs were ligated  
 to Lona-linker IL-Sal4, purified by phenol/chloroform, and  
 separated from free linkers by Centricon 100. Then, the  
 cDNAs were amplified by long-range high fidelity PCR using  
 Ex Taq polymerase (Takara) with a primer Sal4-S. The  
 products were purified by phenol/chloroform and Centricon  
 100. The cDNAs were digested with SalI and NotI enzymes  
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
 The DH10B E. coli host was transformed with the ligation  
 mixture by the standard chemical method. The average  
 insert size is about 2.1 kb. The library was constructed  
 by Yulan Piao (NIA)."

to Lona-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sali and NotI enzymes and cloned into Sali/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 101 a 136 c 119 g 129 t

Query Match 74.9%; Score 271.8; DB 14; Length 485;  
Best Local Similarity 85.6%; Pred. No. 5.9e-69;  
Matches 316; Conservative 0; Mismatches 47; Indels 6; Gaps 1;  
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
Db 35 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 94  
QY 61 ACTTGTCTTCTCTGGGTTTTCACATGACACTTCTGGTATGGGTGTGAGTGGATTGCA 120  
Db 95 ACTTGTCTTCTCTGGGTTTTCACATGACACTTCTGGTATGGGTGTGAGTGGATTGCGT 154  
QY 121 CAGCCCTCAGGAAGGGTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCGC 180  
Db 155 CAGCCCTCAGGAAGGGTCTGGAGTGGCTGGGCACACATTTATTTGGATGATGACAAGCAC 214  
QY 181 TATAACCCATCCCTGAAGAGCGGGTTCAATCTCCAGGATACCTCCAGCAACCAAGGTA 240  
Db 215 TATAACCCATCCCTGAAGAGCGGGTCAATCTCCAGGATACCTCCAGCAACCAAGGTA 274  
QY 241 TTCTCAAGTACACAGTCTGGACATCTGCAGATACCTGCCACATCTACTGTCTCGAAGG 300  
Db 275 TTCTCAAGTACACAGTCTGGACATCTGCAGATACCTGCCACATCTACTGTCTCGGTTG 334  
QY 301 GTCTCTTAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 354  
Db 335 GCCATTATGACGGGGGACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 394  
QY 355 GTCCTCTCA 363  
Db 395 GTCCTCTCA 403

RESULT 12  
BO231128  
LOCUS  
DEFINITION AGENCOURT 7578094 NCI CGAP\_St1 Mus musculus cDNA clone EST 02-MAY-2002  
IMAGE:6051673 5', mRNA sequence.  
BO231128  
ACCESSION BO231128.1 GI:20412528  
VERSION  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NIH-MGC <http://mgi.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM13305 row: o column: 02

High quality sequence stop: 640.  
Location/Qualifiers  
1. 920  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6051673"  
/lab\_host="DH10B (TI-resistant)"  
/clone\_lib="NCI CGAP St1"  
/notes="Organ: stomach; Vector: pCMV-SPORT6; Site 1: Sali; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.77 kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."  
BASE COUNT 205 a 264 c 224 g 222 t  
ORIGIN  
Query Match 74.8%; Score 271.6; DB 13; Length 920;  
Best Local Similarity 85.8%; Pred. No. 8.6e-69;  
Matches 314; Conservative 0; Mismatches 49; Indels 3; Gaps 1;  
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
Db 31 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCTCTCAGTCTG 90  
QY 61 ACTTGTCTTCTCTGGGTTTTCACATGACACTTCTGGTATGGGTGTGAGTGGATTGCA 120  
Db 91 ACTTGTCTTCTCTGGGTTTTCACATGACACTTCTGGTATGGGTGTGAGTGGATTGCGT 150  
QY 121 CAGCCCTCAGGAAGGGTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCGC 180  
Db 151 CAGCCCTCAGGAAGGGTCTGGAGTGGCTGGGCACACATTTATTTGGATGATGACAAGTAC 210  
QY 181 TATAACCCATCCCTGAAGAGCGGGTTTCAATCTCCAGGATACCTCCAGCAACCAAGGTA 240  
Db 211 TATAACCCATCCCTGAAGAGCGGGTCAATCTCCAGGATACCTCCAGCAACCAAGGTA 270  
QY 241 TTCTCAAGTACACAGTCTGGACATCTGCAGATACCTGCCACATCTACTGTCTCGA--- 297  
Db 271 TTCTCAAGTACACAGTCTGGACATCTGCAGATACCTGCCACATCTACTGTCTCGAGCC 330  
QY 298 AGGCTCTCTTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 357  
Db 331 CGATGGTCACTTTCTTTATTGTTAGTATGTTGGGGCGGAGGAGGAGGAGGAGGAGGAGGAG 390  
QY 358 TCCTCA 363  
Db 391 TCCTCA 396

RESULT 13  
BB872138  
LOCUS  
DEFINITION BB872138 RIKEN full-length enriched, adult male accessory axillary lymph node Mus musculus cDNA clone G630034P22 5', mRNA sequence.  
ACCESSION BB872138  
VERSION BB872138.1 GI:17118348  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 379)  
AUTHORS Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)  
JOURNAL Unpublished



## COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura  
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
e mouse tissues.

## FEATURES

source

Location/Qualifiers

```
1..379
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G63003P22"
/sex="male"
/tissue_type="accessory axillary lymph node"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult male
accessory axillary lymph node"
84 a 97 c 93 g 105 t
```

BASE COUNT

ORIGIN

```
Query Match 73.7%; Score 267.6; DB 10; Length 379;
Best Local Similarity 93.6%; Pred. No. 9.1e-68;
Matches 279; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60
Db 79 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 138

Qy 61 ACTTGTTCTTCTGGGTTTCACTGAGCACTTCGGTATGGGTGAGCTGGATCGA 120
Db 139 ACTTGTTCTTCTGGGTTTCACTGAGCACTTCGGTATGGGTGAGCTGGATCGT 198

Qy 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTTACTGGGATGATGACAGCGC 180
Db 199 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTTGGTGGGATGATGATAGTAC 258

Qy 181 TATTAACCATCTCTGAAGACCGGCTTACATCTCCAGGATACCTCCAGCAACCGAGTA 240
Db 259 TATAACCCAGCCCTGAAGAGTGGGCTCAATCTCCAAGGATACCTCCAAACACGAGTA 318

Qy 241 TTCTCAAGATCAACCATGTTGGACACTCGAGATCTGCCACATCTACTGTGTCGAA 298
Db 319 TTCTCAAGATCGCCCAATGTTGGACACTCGAGATCTGCCACATCTACTGTGTCGAA 376
```

RESULT 14

CAS78658

LOCUS

DEFINITION K0726H06-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)

CAS78658

428 bp mRNA

linear

EST 19-NOV-2002

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CDNA library (Long) Mus musculus cDNA clone NIA:K0726H06  
IMAGE:30076121 5', mRNA sequence.

CAS78658

GI:25127049

EST.

Mus musculus (house mouse)

Mus musculus

1 (bases 1 to 428)  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,  
Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.

Systematic Analyses of NIA Mouse Hematopoietic Stem Cell

(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)

Unpublished

Other ESTs: K0726H06-3

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6920, USA

Email: cdna@igsun.grc.nia.nih.gov

Plate: K0726 row: H column: 06

Seq primer: M13 Reverse

High quality sequence stop: 428

POLYA=No.

Location/Qualifiers

```
1..428
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6Ncr"
/db_xref="niaEST:K0726H06-5N"
/db_xref="taxon:10090"
/clone="NIA:K0726H06 IMAGE:30076121"
/tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)"
/dev_stage="Age approx.10 weeks old"
/lab_host="DH10B"
/clone_lib="NIA Mouse Hematopoietic Stem Cell"
(note=vector: pSPORT1 (Invitrogen); Site1: SalI; Site2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001)). [PMID: 11544199]). Total RNAs were  
obtained from Drs. Dennis Taub, Dan Longo (National Cancer  
Institute, USA), Jonathan Keller (National Cancer  
Institute, USA). Double-stranded cDNAs were synthesized  
with an Oligo(dT) primer (Invitrogen):  
5'-PGACTAGTCTAGATCGAGCGCCGCTTTT-3' from  
0.9 ug of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to lone-linker L1-Sal4, purified by phenol/chloroform, and  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer Sal4-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.1 kb. The library was constructed  
by Yulan Piao (NIA)."
```

BASE COUNT

ORIGIN

```
93 a 116 c 108 g 111 t
Query Match 73.2%; Score 265.8; DB 14; Length 428;
Best Local Similarity 87.1%; Pred. No. 3.2e-67;
Matches 304; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

Qy 15 AGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTGACTGTTCTTC 74
Db 1 AGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTGACTGTTCTTC 60
```



further details.  
 e mouse tissues.  
 Location/Qualifiers  
 1. 363  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="G630018N20"  
 /sex="male"  
 /tissue\_type="accessory axillary lymph node"  
 /dev\_stage="adult"  
 /clone\_lib="RIKEN full-length enriched, adult male  
 accessory axillary lymph node"  
 79 a 93 c 90 g 101 t  
 BASE COUNT  
 ORIGIN  
 Query Match 72.3%; Score 262.6; DB 10; Length 363;  
 Best Local Similarity 93.5%; Pred. No. 2.6e-66;  
 Matches 274; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
 QY 1 CAGGTTACTCTGAAGAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60  
 Db 71 CAGGTTACTCTGAAGAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 130  
 QY 61 ACTGTTCTTTCTCTGGGTTTTCACCTGAGCAGTCTCTGGTATGGGTGTGAGCTGGATTGA 120  
 Db 131 ACTGTTCTTTCTCTGGGTTTTCACCTGAGCAGTCTTTGGTATGGGTGTGAGCTGGATTGT 190  
 QY 121 CAGCCTTTCAAGAAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAAAGCG 180  
 Db 191 CAGCCTTTCAAGAAAGGCTCTGGAGTGGCTGGGACACATTTGGTGGATGATGATAAGTAC 250  
 QY 181 TATAACCCATCCCTGAAGAGCCGGTTTCAATCTCAAGGATACCTCCAGCAACACAGGTA 240  
 Db 251 TATAACCCAGCCCTGAAGAGTCCGGCTCACAATCTCAAGGATACCTCCAAAAACCAAGTA 310  
 QY 241 TTCTCTCAAGATCACCAGTGTGGGACACTCCGAGATACCTGCCACATACCTACTCTGTGC 293  
 Db 311 TTCTCTCAAGATCACCAGTGTGGGACACTCCGAGATACCTGCCACATACCTACTCTGTGC 363  
 Search completed: January 14, 2004, 17:46:49  
 Job time : 1468.4 secs

75 TGGGTTTTCACTGAGCATTCTGGTATGGTGTGAGCTGATTCGACAGCCTTCAGGAA 134  
 Db 61 TGGGTTTTCACTGAGCATTCTGGTATGGTGTGAGCTGATTCGACAGCCTTCAGGAA 120  
 QY 135 GGGTCTGAGTGGCTGGGACACATTACTGGGATGATGACAGGCTATAACCCATCCCT 194  
 Db 121 GGGTCTGAGTGGCTGGGACACATTCTGGGATGATGATGATGATGATGATGATGATGAT 180  
 QY 195 GAAGAGCCGGCTTACAACTCCAGGATACCTCCAGCAACAGGATATTCCTCAAGATCAC 254  
 Db 181 GAAGAGTCCGGCTCAAACTCCAGGATACCTCCAGCAACAGGATATTCCTCAAGATCAC 240  
 QY 255 CAGTGTGGACACTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 314  
 Db 241 CAATGTGGACACTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 QY 315 CTATGCTATGGACTACTGGGCTCAAGGACCTCAGTCAACCTCTCTCTCA 363  
 Db 301 TTA---CTTCGATGTCTGGGGCACAGGGACCGGTCAACCGTCTCTCTCA 346

BB870162 363 bp mRNA linear EST 27-NOV-2001  
 BB870162 RIKEN full-length enriched, adult male accessory axillary  
 lymph node Mus musculus cDNA clone G630018N20 5', mRNA sequence.  
 BB870162  
 EST.  
 BB870162.1 GI:17116372  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 363)  
 Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,  
 Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii  
 Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,  
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,  
 Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,  
 Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa  
 A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,  
 Watahiki, A., Yasunishi, A., Muramatsu, M., Hayashizaki, Y.,  
 Watahiki, A., Yasunishi, A., Muramatsu, M., Hayashizaki, Y., et al.  
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.  
 2001)

Unpublished  
 Contact: Yoshinhide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsr.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
 M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura  
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
 Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
 Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 15:55:45 ; Search time 44 Seconds  
(without alignments)  
3641.411 Million cell updates/sec

Title: US-09-759-112A-5

Perfect score: 363

Sequence: 1 cagggtactctgaagagtc.....ctcagtcacgtctctcctca 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCITUS COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	313.4	86.3	483	2	US-08-483-636-3
2	313.4	86.3	483	2	US-08-483-632-3
3	311.8	85.9	423	2	US-08-483-636-9
4	311.8	85.9	423	2	US-08-483-632-9
5	299.2	82.4	738	1	US-08-197-834-6
6	296.4	81.7	417	5	PCT-US95-07372-9
7	291	80.2	418	2	US-08-553-501A-28
8	291	80.2	418	3	US-09-205-231-28
9	261.8	72.1	462	1	US-08-436-463-1
10	250.8	69.1	812	1	US-08-408-133-1
11	250.8	69.1	812	1	US-08-454-683-1
12	250.8	69.1	812	2	US-08-116-778E-16
13	250.8	69.1	812	2	US-08-454-680-1
14	250.8	69.1	812	2	US-08-438-562-16
15	250.8	69.1	812	2	US-08-483-528B-16
16	250.8	69.1	812	3	US-08-673-799C-16
17	250.8	69.1	812	4	US-09-393-385B-16
18	250.8	69.1	812	4	US-09-225-322B-1
19	250.8	69.1	812	4	US-09-764-304-1
20	191.4	52.7	423	4	US-08-561-309-50
21	190.6	52.5	423	2	US-08-345-321-9
22	190.2	52.4	613	3	US-08-545-809A-5
23	185.4	51.1	418	3	US-08-553-501A-58
24	185.4	51.1	418	3	US-09-205-231-58
25	185.4	51.1	1607	3	US-09-049-672A-14
26	183.8	50.6	418	2	US-08-553-501A-60
27	183.8	50.6	418	3	US-09-205-231-60

28	181.2	49.9	546	3	US-08-545-809A-26	Sequence 26, Appl
29	172.6	47.5	630	3	US-08-545-809A-10	Sequence 10, Appl
30	171	47.1	423	2	US-08-483-636-11	Sequence 11, Appl
31	171	47.1	423	2	US-08-483-632-11	Sequence 11, Appl
32	168.4	46.4	646	4	US-09-702-705-1113	Sequence 1113, Ap
33	168.4	46.4	646	4	US-09-736-457-1113	Sequence 1113, Ap
34	165	45.5	714	4	US-09-142-974B-2	Sequence 2, Appl1
35	165	45.5	1173	4	US-09-142-974B-4	Sequence 4, Appl1
36	163.2	45.0	378	1	US-08-488-376-15	Sequence 15, Appl
37	163.2	45.0	378	2	US-08-634-223-15	Sequence 15, Appl
38	163.2	45.0	378	2	US-08-634-224-15	Sequence 15, Appl
39	163.2	45.0	378	2	US-08-634-400-15	Sequence 15, Appl
40	163.2	45.0	378	2	US-08-635-878-15	Sequence 15, Appl
41	163.2	45.0	378	2	US-08-770-057-15	Sequence 15, Appl
42	163.2	45.0	378	3	US-09-335-697B-15	Sequence 15, Appl
43	163.2	45.0	378	4	US-09-335-697B-15	Sequence 15, Appl
44	163.2	45.0	378	4	US-09-740-002-15	Sequence 15, Appl
45	163.2	45.0	1428	1	US-08-488-376-19	Sequence 19, Appl

## ALIGNMENTS

RESULT 1  
US-08-483-636-3  
; Sequence 3, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 483 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown

```

; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64..483
; US-08-483-636-3
;
; Query Match
; Best Local Similarity 86.3%; Score 313.4; DB 2; Length 483;
; Mismatches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
;
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 60
DB 121 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 180
QY 61 ACTGTTCTTTCTCTGGGTTTTCACGTGACACTCTGGTATGGGTGTGAGTGGATTGGA 120
DB 181 ACTGTTCTTTCTCTGGGTTTTCACGTGACACTCTGGTATGGGTGTGAGTGGATTGGA 240
QY 121 CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCC 180
DB 241 CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCC 300
QY 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACCCAGGTA 240
DB 301 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACCCAGGTA 360
QY 241 TTCTCAAGATCACCAGTGTGGAGTGGCTGGGCACATCTACTGTGCTCGAAGG 300
DB 361 TTCTCAAGATCACCAGTGTGGAGTGGCTGGGCACATCTACTGTGCTCGAAGG 420
QY 301 GTCTCTTAACCTGCTATGCTATGAGTCTGGGTCAGGATCTGGGTCAGGATCTCC 360
DB 421 GAGACTGTGTTCTACTGTTGATGTTCTGGGTCAGGATCTGGGTCAGGATCTCC 480
QY 361 TCA 363
DB 481 TCA 483
;
RESULT 2
US-08-483-632-3
; Sequence 3, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64..483
; US-08-483-632-3
;
; Query Match
; Best Local Similarity 86.3%; Score 313.4; DB 2; Length 483;
; Mismatches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
;
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 60
DB 121 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGCGACCCCTCCAGACCCCTCAGTCTG 180
QY 61 ACTGTTCTTTCTCTGGGTTTTCACGTGACACTCTGGTATGGGTGTGAGTGGATTGGA 120
DB 181 ACTGTTCTTTCTCTGGGTTTTCACGTGACACTCTGGTATGGGTGTGAGTGGATTGGA 240
QY 121 CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCC 180
DB 241 CAGCCTTCAGGAAAGGTTCTGGAGTGGCTGGGCACACATTTACTGGGATGATGACAAGCC 300
QY 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACCCAGGTA 240
DB 301 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACCCAGGTA 360
QY 241 TTCTCAAGATCACCAGTGTGGAGTGGCTGGGCACATCTACTGTGCTCGAAGG 300
DB 361 TTCTCAAGATCACCAGTGTGGAGTGGCTGGGCACATCTACTGTGCTCGAAGG 420
QY 301 GTCTCTTAACCTGCTATGCTATGAGTCTGGGTCAGGATCTGGGTCAGGATCTCC 360
DB 421 GAGACTGTGTTCTACTGTTGATGTTCTGGGTCAGGATCTGGGTCAGGATCTCC 480
QY 361 TCA 363
DB 481 TCA 483
;
RESULT 3
US-08-483-636-9
; Sequence 9, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA

```

ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483.636  
FILING DATE: 14-OCT-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..423  
US-08-483-636-9

Query Match 85.9%; Score 311.8; DB 2; Length 423;  
Best Local Similarity 91.2%; Pred. No. 2.4e-98;  
Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 1 CAGGTTACTCTGAAGAGCTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 61 CAGGTTACCTTGAAGAGCTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 120  
QY 61 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGTATGGGTGTGAGCTGGATTCTGA 120  
DB 121 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGTATGGGTGTGAGCTGGATTCTGT 180  
QY 121 CAGCCTTCAGAAAGGGTCTGGAGTGGCTGCACACATTTTCTGGGATGATGACAAAGCGC 180  
DB 181 CAGCCTTCAGAAAGGGTCTGGAGTGGCTGCACACATTTTCTGGGATGATGACAAAGCGC 240  
QY 181 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 240  
DB 241 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 300  
QY 241 TTCTCAGATCACCAGTGTGGACACTGAGATATCTGCACATCTACTGTGTCTGGAAGG 300  
DB 301 TTCTCAGATCACCAGTGTGGACACTGAGATATCTGCACATCTACTGTGTCTGGAAGG 360  
QY 301 GTCTCTCTAACTGCTATGCTATGACTTCTGGGGTCAAGGAACCTCAGTCACCGTCTCC 360  
DB 361 GAGACTGTGTCTACTTGTGTTCTGATGTTCTGGGGCGGACGAGGACACCGTCTCC 420  
QY 361 TCA 363  
DB 421 TCA 423  
RESULT 4  
US-08-483-632-9

Sequence 9, Application US/08483632  
Patent No. 5928904  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
APPLICANT: Gross, Mitchell S.  
APPLICANT: Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P.O. Box 1539 / UW2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483.632  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..423  
US-08-483-632-9

Query Match 85.9%; Score 311.8; DB 2; Length 423;  
Best Local Similarity 91.2%; Pred. No. 2.4e-98;  
Matches 331; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 1 CAGGTTACTCTGAAGAGCTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 61 CAGGTTACCTTGAAGAGCTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 120  
QY 61 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGTATGGGTGTGAGCTGGATTCTGA 120  
DB 121 ACTTGTTCTTCTCTGGGTTTCTACTGAGCACTTCTGTATGGGTGTGAGCTGGATTCTGT 180  
QY 121 CAGCCTTCAGAAAGGGTCTGGAGTGGCTGCACACATTTTCTGGGATGATGACAAAGCGC 180  
DB 181 CAGCCTTCAGAAAGGGTCTGGAGTGGCTGCACACATTTTCTGGGATGATGACAAAGCGC 240  
QY 181 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 240  
DB 241 TATAACCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGCAACAGGTA 300

241	TTCTCTCAAGATCACGAGTGTGGACACTCGAGATACTGCCACATACACTGTGTCTCGAAGG	300
QY		
301	TTCTCTCAAGATCACGAGTGTGGACACTGTGGCACAATCTACTGTGTCTCGAAGA	360
Db		
301	GTCTCTCTCAACTGGCCTATGCTATCGACTACTGGGGTCAAGGAACCTTCAGTCACCGTCTCC	360
QY		
361	GAGACTGTGTCTACTGTGTACTTTCGATGTCTGGGGCGCAGGACCAAGTTCACCGTCTCC	420
Db		
361	TCA	363
QY		
421	TCA	423
Db		

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999

```

61 ACTTGTCTTCTCTGGGTTTTCACTGAGCACATTTCTGGTATGGGTGTGAGCTGGATTCTGA 120  
Db ACTTGTCTTCTCTGGGTTTTCACTGAGCACATTTCTGGTATGGGTGTGAGCTGGATTCTGT 486  
QY 121 CAGCCTTTCAGAGAAAGGGTCTGGAGTGGCTGGCCACACATTTTACTGGGATGATGACAAGCGC 546  
Db 487 CAGCCTTTCAGAGAAAGGGTCTGGAGTGGCTGGCCACACATTTTATTTGGGATGATGACAAACAC 546  
QY 181 TATAACCATCCCTGAAGAGCGCGCTTACAAATCTCAAAGGATACCTCCAGCAACCAAGGTA 240  
Db 547 TATAACCATCCCTGAAGAGCGCGCTCACAATCTCCAAGGATACCTCCACCAACCAAGGTA 606  
QY 241 TTCTCTCAGATCACAGTGTGGACACTCGAGATACTGCCACATACTCTGTCTCGAAG- 299  
Db 607 TTCTCTCAGATCACAGTGTGGACACTCGAGATACTGCCACATACTCTGTCTCGAAG 666  
QY 300 -----GGTCTCTTAACCTGCCTATGCTATGGACTACTGGGCTCAAGGAACCTCAGTC 351  
Db 667 AGTCTCTATGGTAAATGGGGGGACTATGCTATGGACTACTGGGCTCAAGGAACCTCAGTC 726  
QY 352 ACCGTCTCTCTCA 363  
Db 727 ACCGTCTCTCTCA 738

RESULT 6  
PCT-US95-07372-9  
; Sequence 9, Application PC/TUS9507372  
; GENERAL INFORMATION:  
; APPLICANT: Oklahoma Medical Research Foundation  
; TITLE OF INVENTION: Calcium Binding Recombinant  
; TITLE OF INVENTION: Antibody Against Protein C  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/07372  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMRF106CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 417 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: 1..57  
; OTHER INFORMATION: /note="Signal peptide encoded by  
; nucleotides 1 through 57."

FEATURE:  
NAME/KEY: misc feature  
LOCATION: 58, 417  
OTHER INFORMATION: /note= "Mature peptide encoded by  
OTHER INFORMATION: nucleotides 58 through 417."  
PCT-US95-07372-9

Query Match 81.7%; Score 296.4; DB 5; Length 417;  
Best Local Similarity 90.6%; Pred. No. 5.1e-93;  
Matches 328; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 58 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 117  
QY 61 ACTTGTCTCTCTCTGGTTTTCACAGCAGCCTCTGGTATGGTCTGAGCTGGATTGCA 120  
DB 118 ACTTGTCTCTCTCTGGTTTTCACAGCAGCCTCTGGTATGGTCTGAGCTGGATTGCT 177  
QY 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180  
DB 178 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 237  
QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 240  
DB 238 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 297  
QY 241 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTCTGGAAGG 300  
DB 298 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTCTGGAATG 357  
QY 301 GTCTCTCTAACTCCCTATGCTATGGACTACTGGGGTCAAGGAACTCAGTCAACCGTCTCC 360  
DB 358 ATGGAT---GATTACGACGCTATGGACTACTGGGGTCAAGGAACTCAGTCAACCGTCTCC 414  
QY 361 TC 362  
DB 415 TC 416

RESULT 7  
US-08-553-501A-28  
Sequence 28, Application US/08553501A  
Patent No. 5856135  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: HIRATA, Yuichi  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,501A  
FILING DATE: 20-FEB-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993

ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 418 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..417  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 1..417  
US-08-553-501A-28

Query Match 80.2%; Score 291; DB 2; Length 418;  
Best Local Similarity 89.5%; Pred. No. 3.8e-91;  
Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 58 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 117  
QY 61 ACTTGTCTCTCTCTGGTTTTCACAGCAGCCTCTGGTATGGTCTGAGCTGGATTGCA 120  
DB 118 ACTTGTCTCTCTCTGGTTTTCACAGCAGCCTCTGGTATGGTCTGAGCTGGATTGCT 177  
QY 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180  
DB 178 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGATAAGTAC 237  
QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 240  
DB 238 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 297  
QY 241 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTCTGGAAGG 300  
DB 298 TTCTCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATACCTACTGTCTGGAATG 357  
QY 301 GTCTCTCTAACTCCCTATGCTATGGACTACTGGGGTCAAGGAACTCAGTCAACCGTCTCC 360  
DB 358 GAGGAT---TACGACGAGGCTATGGACTACTGGGGTCAAGGAACTCAGTCAACCGTCTCC 414  
QY 361 TCA 363  
DB 415 TCA 417

RESULT 8  
US-09-205-231-28  
Sequence 28, Application US/09205231  
Patent No. 6121423  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: HIRATA, Yuichi  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 30-MAY-1994  
APPLICATION NUMBER: US/09/205,231  
CLASSIFICATION:  
PRIORITY INFORMATION:  
PRIORITY APPLICATION DATA: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 418 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..417  
FEATURE:  
NAME/KEY: mat peptide  
LOCATION: 1..417  
US-09-205-231-28

Query Match 80.2%; Score 291; DB 3; Length 418;  
Best Local Similarity 89.5%; Pred. No. 3.8e-91;  
Matches 325; Conservative 0; Mismatches 35; Indels 3; Gaps 1;  
QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCGCCCTCCAGACCCCTCAGTCTG 60  
DB 58 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCGCCCTCCAGACCCCTCAGTCTG 117  
QY 61 ACTTGTTCTTTCTCTGGGTTTCTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGGA 120  
DB 118 ACTTGTTCTTTCTCTGGGTTTCTGAGCACTTCTGGTATGACCGTAGGCTGGATTGCT 177  
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180  
DB 178 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGGACACATTTGGTGAATGATGATAGTAC 237  
QY 181 TATAACCCATCCCTGGAAGAGCGGCTTACAACTCTCAAGGATACCTCCAGCAACACAGGTA 240  
DB 238 TATAACCCAGCCCTGAAGAGCGGCTTACAACTCTCAAGGATACCTCCAGCAACACAGGTA 297  
QY 241 TTCTCTAAGATACCAAGTGGGACACTGCGAGATCTGCGGACATATCTGTTGTCGAAGG 300  
DB 298 TTCTCTAAGATCGGAGTGGTCTGAGTGGCTGAGTGGTCTGAGTGGTCTGAGTGGTCTG 357  
QY 301 GTCTCTTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
DB 358 GAGAT---TACGACGAAGCTATGAGTACTTGGGTCAAGGAACCTCAGTACCCGCTCTCC 414  
QY 361 TCA 363  
DB 415 TCA 417

RESULT 9

US-08-436-463-1  
Sequence 1, Application US/08436463  
Patent No. 5760185  
GENERAL INFORMATION:  
APPLICANT: KIMACHI, Kazuhiko  
APPLICANT: MAEDA, Hiroaki  
APPLICANT: NISHIYAMA, Kiyoto  
APPLICANT: TOKIYOSHI, Sachio  
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,463  
FILING DATE: 26-JUN-1995  
CLASSIFICATION: 536  
PRIORITY INFORMATION:  
PRIORITY APPLICATION DATA:  
FILING DATE: 28-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: KIMACHI=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 462 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 21..449  
US-08-436-463-1

Query Match 72.1%; Score 261.8; DB 1; Length 462;  
Best Local Similarity 92.6%; Pred. No. 5.3e-81;  
Matches 275; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
QY 1 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCGCCCTCCAGACCCCTCAGTCTG 60  
DB 78 CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGCGCCCTCCAGACCCCTCAGTCTG 137  
QY 61 ACTTGTTCTTTCTCTGGGTTTCTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGGA 120  
DB 138 ACTTGTTCTTTCTCTGGGTTTCTGAGCACTTCTGGTATGGGTGTGAGCTGGATTGCT 197  
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180  
DB 198 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGGACACATTTGGTGGGATGATGTCAGCGC 257  
QY 181 TATAACCCATCCCTGGAAGAGCGGCTTACAACTCTCAAGGATACCTCCAGCAACACAGGTA 240  
DB 258 TATAACCCAGCCCTGAAGAGCGGCTTACAACTCTCAAGGATACCTCCAGCAACACAGGTA 317  
QY 241 TTCTCTAAGATCACCAGTGTGGACACTCGAGATACTGCCACATACTACTGTGCTCGA 297  
DB 318 TTCTCTAAGATCGGAGTGGACACTCGAGATACTGCCACATATTTTGTGTTGGA 374

```

RESULT 10
US-08-408-133-1
; Sequence 1, Application US/08408133
; Patent No. 5750078
; GENERAL INFORMATION:
; APPLICANT: SHITARA, Kenya
; APPLICANT: HANAI, No. 5750078uo
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: MIYAJI, Hirohisa
; APPLICANT: KUWANA, Yoshinisa
; TITLE OF INVENTION: Process for Producing Humanized Chimera
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Nixon & Vandethye, P.C.
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,133
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,178
; FILING DATE:
; APPLICATION NUMBER: US 07/947,674
; FILING DATE: 17-SEPT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, Arthur R
; TELEPHONE: (703)816-4000
; TELEFAX: (803)816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ORIGINAL SOURCE:
; STRAIN: Hybridoma KM50
; FEATURE:
; NAME/KEY: TATA signal
; LOCATION: 256..262
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 441..806
; OTHER INFORMATION: /product= "RAT IMMUNOGLOBULIN HEAVY
; OTHER INFORMATION: CHAIN VARIABLE REGION"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 300..440
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(300..345, 429..806)
; OTHER INFORMATION:
;
; US-08-408-133-1
; Query Match 69.1%; Score 250.8; DB 1; Length 812;
; Best Local Similarity 82.2%; Pred. No. 4.6e-77;
; Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

```

```

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGAGCCCTCAGTCTG 60
Db 441 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGAGCCCTCAGTCTG 500
QY 61 ACTTGTCTCTTCTCTGGGTTTTCACCTGAGCACCTTCTGGTATGGGTGTGAGCTGGATTGGA 120
Db 501 ACTTGTCTCTTCTCTGGGTTTTCACCTGAGCACCTTCTGGTATGGGTGTGAGCTGGATTGGA 560
QY 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTTACTGGGATGATGACAGCCG 180
Db 561 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGGACACATTTTACTGGGATGATGATGATGATGAT 620
QY 181 TATAAACCATCCCTGAAGAGCCGCTTACAACTCTCAAGGATACCTCCAGAACACACAGGTA 240
Db 621 TACATTCATCTCTGAAACACCGCTCACAACTCTCAAGGACACCTCCACACACAGCA 680
QY 241 TTCCTCAAGATCACAGTGTGGACACTCGAGATATGCGCATATCTACTGTGTGGAAGG 300
Db 681 TTCCTCAAGATCACAAATATGGACACTGCGCATATCTACTGTGTGGAAGG 740
QY 301 GTCTCTCTAACTGCTATGCTA---TGGACTACTGGGTCAAGGAACCTCAGTCACCGTC 357
Db 741 GGGCTACGGAGGTATAGTACGCTTTGATTCTGGGCGCACCGAGTCTAGTGTGATGTC 800
QY 358 TCCTCA 363
Db 801 TCCTCA 806

```

```

RESULT 11
US-08-454-683-1
; Sequence 1, Application US/08454683
; Patent No. 5807548
; GENERAL INFORMATION:
; APPLICANT: SHITARA, Kenya
; APPLICANT: HANAI, No. 5807548uo
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: MIYAJI, Hirohisa
; APPLICANT: KUWANA, Yoshinisa
; TITLE OF INVENTION: Process for Producing Humanized Chimera
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Nixon & Vandethye, P.C.
; STREET: No. 5807548th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,683
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,133
; FILING DATE:
; APPLICATION NUMBER: US 08/292,178
; FILING DATE:
; APPLICATION NUMBER: US 07/947,674
; FILING DATE: 17-SEPT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, Arthur R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (803)816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:

```



```

SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ORIGINAL SOURCE:
STRAIN: Hybridoma KM50
FEATURE:
NAME/KEY: TATA signal
LOCATION: 256..262
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat peptide
LOCATION: 441..806
OTHER INFORMATION: /product= "RAT IMMUNOGLOBULIN HEAVY
OTHER INFORMATION: CHAIN VARIABLE REGION"
FEATURE:
NAME/KEY: sig peptide
LOCATION: 300..440
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: join(300..345, 429..806)
OTHER INFORMATION:
US-08-454-683-1
Query Match
Best Local Similarity 69.1%; Score 250.8; DB 1; Length 812;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 CAGGTTACTCTCAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTCAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTTCTTTCTCTGGGTTTTCACGTGACACTTCTGGTATGGGTGAGTGGATTGGA 120
DB 501 ACTTGTTCTTTCTCTGGGTTTTCACGTGACACTTATGGTATGTGTGGGCTGGATTCTG 560
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACATTTACTTGGGATGATGACCAAGCGC 180
DB 561 CAGTCTTCAGGAAGGGTCTGGAGTGGCTGGCACATTTACTTGGGATGATGACCAAGCGC 620
QY 181 TATAACCCATCCTGAGAGCCGGCTTACAATCTCCAGGATACCTCCAGCAACCAAGCA 240
DB 621 TACAATCCATCCTGAGAAACCGGCTCAAAATCTCCAGGACACCTCCCAACCAAGCA 680
QY 241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATATCTACTGTCTGGAAGG 300
DB 681 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATATCTACTGTCTGGAAGG 740
QY 301 GTCTCTTAAGTCCCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCAACCGTC 357
DB 741 GGGGCTACGAGGGTATAGTGGCTTTGATTACTGGGGCCACGGAGTCATGGTCAACAGTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

```

```

RESULT 12
US-08-116-778E-16
Sequence 16, Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHITHISA
APPLICANT: HASEGAWA, MANORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES

```

```

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYZE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: HYBRIDOMA KM50
FEATURE:
NAME/KEY: TATA signal
LOCATION: 261..267
US-08-116-778E-16

```

```

Query Match
Best Local Similarity 82.2%; Pred. No. 4.6e-77;
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 CAGGTTACTCTCAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 60
DB 441 CAGGTTACTCTCAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTTCTTTCTCTGGGTTTTCACGTGACACTTCTGGTATGGGTGAGTGGATTGGA 120
DB 501 ACTTGTTCTTTCTCTGGGTTTTCACGTGACACTTATGGTATGTGTGGGCTGGATTCTG 560
QY 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACATTTACTTGGGATGATGACCAAGCGC 180
DB 561 CAGTCTTCAGGAAGGGTCTGGAGTGGCTGGCACATTTACTTGGGATGATGACCAAGCGC 620
QY 181 TATAACCCATCCTGAGAGCCGGCTTACAATCTCCAGGATACCTCCAGCAACCAAGCA 240
DB 621 TACAATCCATCCTGAGAAACCGGCTCAAAATCTCCAGGACACCTCCCAACCAAGCA 680
QY 241 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATATCTACTGTCTGGAAGG 300
DB 681 TTCCTCAAGATCACCAGTGTGGACACTCGAGATACCTGCCACATATCTACTGTCTGGAAGG 740
QY 301 GTCTCTTAAGTCCCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCAACCGTC 357
DB 741 GGGGCTACGAGGGTATAGTGGCTTTGATTACTGGGGCCACGGAGTCATGGTCAACAGTC 800
QY 358 TCCTCA 363
DB 801 TCCTCA 806

```

```

RESULT 13
US-08-454-680-1

```

```

; Sequence 1, Application US/08454680
; Patent No. 5866692
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA
; TITLE OF INVENTION: ANTIBODY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,680
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/408,133
; FILING DATE: 21-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,178
; FILING DATE: 17-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/947,674
; FILING DATE: 17-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-238375
; FILING DATE: 18-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 249-74
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: TATA_signal
; LOCATION: 256..262
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 441..806
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 300..440
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(300..345, 430..806)
; US-08-454-680-1
;
; Query Match 69.1%; Score 250.8; DB 2; Length 812;
; Best Local Similarity 82.2%; Pred. No. 4.6e-77;
; Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
;
; 1 CAGGTACTCTGAAGAGTCTGGGATATTGCGCCCTCCAGACCCCTCAGTCTG 60
|||||

```

```

Db 441 CAGGTACTCTGAAGAGTCTGGGATATTGCGCCCTCCAGACCCCTCAGTCTG 500
QY 61 ACTTGTCTCTCTCTGGGTTTCTACTGAGCACTTCTGGTATGGGTGAGCTGGATTGGA 120
Db 501 ACTTGTCTCTCTCTGGGTTTCTACTGAGCACTTATGGTATGGTGGGCTGGATTCTGT 560
QY 121 CAGCTTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGGC 180
Db 561 CAGTCTTCAGGGAAGGGTCTGGAGTGGCTGGCAACCGTTTGGTGGAGTGGTCTAGTAC 620
QY 181 TATAACCCATCCCTGAAGAGCGCGCTTACAACTTCCAAAGGATACCTCCAGCAACAGGTA 240
Db 621 TACAATCCATCTCTGAAAAACCGGCTCACAACTCTCCAAGGACACCTCCAAACCAAGCA 680
QY 241 TTCTCTCAAGATCACCAAGTGTGGACACTCGAGATATCGGATATCTCCATATCTACTGTGCTCGAAGG 300
Db 681 TTCTCTCAAGATCACCAATATGGACACTGCAGATATCTCCATATCTACTGTGCTGGGAGA 740
QY 301 GTCTCTTAAGTGCCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCAACGTC 357
Db 741 GGGGCTACGGAGGGTATAGTCAGCTTTGATTACTGGGGCCACGAGTCAATGTTCAAGTC 800
QY 358 TCCTCA 363
Db 801 TCCTCA 806
;
RESULT 14
US-08-438-562-16
; Sequence 16, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

```

MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE: HYBRIDOMA KM50  
FEATURE: TATA signal  
NAME/KEY: TATA signal  
LOCATION: 261..267  
US-08-438-562-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;  
Best Local Similarity 82.2%; Pred. No. 4.6e-77;  
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 441 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 500  
QY 61 ACTTGTCTCTTCTCTGGTTTTCACGTGACACTCTCTGGTATGGGTGAGCTGGATTGGA 120  
DB 501 ACTTGTCTCTTCTCTGGTTTTCACGTGACACTCTCTGGTATGGGTGAGCTGGATTGGA 560  
QY 121 CAGCCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAAGCGC 180  
DB 561 CAGTCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAAGCGC 620  
QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAGGATACCTCCAGCAACCAAGCA 240  
DB 621 TACAATCCATCTCTGAAGAAACCGGCTTACAATCTCCAGGATACCTCCAGCAACCAAGCA 680  
QY 241 TTCTCTCAAGATCACCAGTGTGGACACTCGACATACCTGCCACATACCTACTGTCTCGAAGG 300  
DB 681 TTCTCTCAAGATCACCAGTGTGGACACTCGACATACCTGCCACATACCTACTGTCTCGAAGG 740  
QY 301 GTCTCTCTAACTCCCTATGCTA---TGGACTACTGGGGTCAAGGAACTTCAGTCAACGTC 357  
DB 741 GGGGCTACGGAGGGTATAGTGGCTTTGATTACTGGGGCCACGGAGTCATGCTCAAGTC 800  
QY 358 TCCTCA 363  
DB 801 TCCTCA 806

RESULT 15  
US-08-483-528B-16  
Sequence 16, Application US/08483528B  
Patent No. 593532  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUWANA, YOSHIIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHIE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483, 528B  
FILING DATE: 07-JUN-95  
CLASSIFICATION: 536  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 812 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE: HYBRIDOMA KM50  
FEATURE: TATA signal  
NAME/KEY: TATA signal  
LOCATION: 261..267  
US-08-483-528B-16

Query Match 69.1%; Score 250.8; DB 2; Length 812;  
Best Local Similarity 82.2%; Pred. No. 4.6e-77;  
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 441 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 500  
QY 61 ACTTGTCTCTTCTCTGGTTTTCACGTGACACTCTCTGGTATGGGTGAGCTGGATTGGA 120  
DB 501 ACTTGTCTCTTCTCTGGTTTTCACGTGACACTCTCTGGTATGGGTGAGCTGGATTGGA 560  
QY 121 CAGCCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAAGCGC 180  
DB 561 CAGTCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAAGCGC 620  
QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCCAGGATACCTCCAGCAACCAAGCA 240  
DB 621 TACAATCCATCTCTGAAGAAACCGGCTTACAATCTCCAGGATACCTCCAGCAACCAAGCA 680  
QY 241 TTCTCTCAAGATCACCAGTGTGGACACTCGACATACCTGCCACATACCTACTGTCTCGAAGG 300  
DB 681 TTCTCTCAAGATCACCAGTGTGGACACTCGACATACCTGCCACATACCTACTGTCTCGAAGG 740  
QY 301 GTCTCTCTAACTCCCTATGCTA---TGGACTACTGGGGTCAAGGAACTTCAGTCAACGTC 357  
DB 741 GGGGCTACGGAGGGTATAGTGGCTTTGATTACTGGGGCCACGGAGTCATGCTCAAGTC 800  
QY 358 TCCTCA 363  
DB 801 TCCTCA 806

Search completed: January 14, 2004, 17:48:16  
Job time : 47 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 16:03:20 ; Search time 215.81 Seconds  
(without alignments)  
5928.789 Million cell updates/sec

Title: US-09-759-112A-5

Perfect score: 363

Sequence: 1 caggttactctgaagagtc.....ctcagtcaccgtctctctca 363

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	363	100.0	363	11	US-09-759-112A-5
2	363	100.0	363	11	US-09-759-112A-6
3	313.4	86.3	483	10	US-09-879-461-3
4	311.8	85.9	423	10	US-09-879-461-9
5	311.8	85.9	426	13	US-10-010-942B-15
6	299	82.4	369	11	US-09-995-529-11
7	284.4	78.3	465	9	US-09-881-823-7
8	270.8	74.6	357	12	US-10-323-903-4
9	250.8	69.1	812	9	US-09-784-304-1
10	250.8	69.1	812	13	US-10-166-626-1
11	250.8	69.1	812	15	US-10-195-752-16
12	250.8	69.1	812	15	US-10-265-713-1
13	191.4	52.7	423	13	US-10-255-478-50
14	183	50.4	759	13	US-10-072-301-22
15	183	50.4	759	13	US-10-072-301-30

16	183	50.4	759	13	US-10-071-866-22	Sequence 22, Appl
17	183	50.4	759	13	US-10-071-866-30	Sequence 30, Appl
18	183	50.4	759	13	US-10-360-828-22	Sequence 22, Appl
19	183	50.4	759	13	US-10-360-828-30	Sequence 30, Appl
20	182.6	50.3	1625	12	US-10-108-260A-2241	Sequence 2241, Ap
21	180.4	49.7	1557	13	US-10-325-108A-9	Sequence 9, Appl
22	179.2	49.4	288	11	US-09-995-529-15	Sequence 15, Appl
23	178.6	49.2	666	11	US-09-972-656-69	Sequence 69, Appl
24	173.4	47.8	759	13	US-10-072-301-16	Sequence 16, Appl
25	173.4	47.8	759	13	US-10-071-866-16	Sequence 16, Appl
26	173.4	47.8	759	13	US-10-360-828-16	Sequence 16, Appl
27	172	47.4	684	11	US-09-972-656-83	Sequence 83, Appl
28	171.8	47.3	759	13	US-10-072-301-24	Sequence 24, Appl
29	171.8	47.3	759	13	US-10-071-866-24	Sequence 24, Appl
30	171.8	47.3	759	13	US-10-360-828-24	Sequence 24, Appl
31	171	47.1	423	10	US-09-879-461-11	Sequence 11, Appl
32	168.4	46.4	646	10	US-09-736-457-1113	Sequence 1113, Ap
33	168.4	46.4	646	10	US-09-902-941-1113	Sequence 1113, Ap
34	168.4	46.4	646	10	US-09-849-626-1113	Sequence 1113, Ap
35	168.4	46.4	646	13	US-10-113-872-1113	Sequence 1113, Ap
36	168.4	46.4	646	15	US-10-017-754-1113	Sequence 1113, Ap
37	165	45.5	714	8	US-08-940-544-4	Sequence 4, Appl
38	165	45.5	714	13	US-10-075-947A-2	Sequence 2, Appl
39	165	45.5	1173	13	US-10-075-947A-4	Sequence 4, Appl
40	163.2	45.0	378	9	US-09-740-002-15	Sequence 15, Appl
41	163.2	45.0	378	12	US-10-384-356-15	Sequence 15, Appl
42	163.2	45.0	1428	9	US-09-740-002-19	Sequence 19, Appl
43	163.2	45.0	1428	12	US-10-384-356-19	Sequence 19, Appl
44	162	44.6	1446	13	US-10-409-938-22	Sequence 22, Appl
45	160.2	44.1	454	10	US-09-797-941A-1	Sequence 1, Appl

## ALIGNMENTS

## RESULT 1

US-09-759-112A-5  
; Sequence 5, Application US/09759112A  
; Publication No. US20030100741A1  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Sybille  
; APPLICANT: Kohler, Heinz  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT ANTI-IDIOTYPIC ANTIBODY 1P7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE  
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1P7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE  
; TITLE OF INVENTION: ANTIBODIES  
; FILE REFERENCE: 200-013  
; CURRENT APPLICATION NUMBER: US/09/759,112A  
; CURRENT FILING DATE: 2001-01-11  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 363  
; TYPE: DNA  
; ORGANISM: mouse  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)...(362)  
; OTHER INFORMATION: 1P7 VH chain gene  
US-09-759-112A-5

Query Match 100.0%; Score 363; DB 11; Length 363;  
Best Local Similarity 100.0%; Pred. No. 1.5e-114;  
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG	60
DB	1	CAGGTACTCTGAAGAGTCTGGCCCTGGGATATTGACGCCCTCCAGACCCCTCAGTCTG	60
QY	61	ACTGTGTTCTCTCGGGTCTTCTACTGAGCACTTCTGGTATGGGTGAGTGTGATTCGA	120
DB	61	ACTGTGTTCTCTCGGGTCTTCTACTGAGCACTTCTGGTATGGGTGAGTGTGATTCGA	120
QY	121	CAGCCTTCAGGNAAGGTCGTGGAGTGGCTGGCGACACATTTACTGGGATGATGACAGCGC	180

```
Db 121 CAGCCTTGAAGAGGCTCTGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180
Qy 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACAGGTA 240
Db 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACAGGTA 240
Qy 241 TTCTCTCAAGATCACCAGTGTGACACTCTGAGATCTGCCACATACCTACTGTGCTCGAAGG 300
Db 241 TTCTCTCAAGATCACCAGTGTGACACTCTGAGATCTGCCACATACCTACTGTGCTCGAAGG 300
Qy 301 GTCTCTTAACCTGCTATGACTACTGGGTCAAGGAACCTCAGTCAACCTCTCC 360
Db 301 GTCTCTTAACCTGCTATGACTACTGGGTCAAGGAACCTCAGTCAACCTCTCC 360
Qy 361 TCA 363
Db 361 TCA 363

RESULT 2
US-09-759-112a-6
; Sequence 6, Application US/09759112a
; Publication No. US20030100741A1
; GENERAL INFORMATION:
; APPLICANT: Mueller, Sybille
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1P7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 200-013
; CURRENT APPLICATION NUMBER: US/09/759,112a
; CURRENT FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 363
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(363)
; OTHER INFORMATION: 1P7 VH chain gene
US-09-759-112a-6

Query Match 100.0%; Score 363; DB 11; Length 363;
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGTTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGGCCCTCCAGACCCCTCAGTCTG 60
Db 1 CAGTTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGGCCCTCCAGACCCCTCAGTCTG 60
Qy 61 ACTTGTCTTTCTCTGGTCTTCACTGAGCACTTCTGGTATGGGTGAGCTGGATTGGA 120
Db 61 ACTTGTCTTTCTCTGGTCTTCACTGAGCACTTCTGGTATGGGTGAGCTGGATTGGA 120
Qy 121 CAGCCTTCAGAAAGGCTCTGGATGGCTGGACACATTTACTGGGATGATGACAGCGC 180
Db 121 CAGCCTTCAGAAAGGCTCTGGATGGCTGGACACATTTACTGGGATGATGACAGCGC 180
Qy 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACAGGTA 240
Db 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCAAGGATACCTCCAGCAACAGGTA 240
Qy 241 TTCTCTCAAGATCACCAGTGTGACACTCTGAGATCTGCCACATACCTACTGTGCTCGAAGG 300
Db 241 TTCTCTCAAGATCACCAGTGTGACACTCTGAGATCTGCCACATACCTACTGTGCTCGAAGG 300
Qy 301 GTCTCTTAACCTGCTATGACTACTGGGTCAAGGAACCTCAGTCAACCTCTCC 360
Db 301 GTCTCTTAACCTGCTATGACTACTGGGTCAAGGAACCTCAGTCAACCTCTCC 360
```

```
Qy 361 TCA 363
Db 361 TCA 363

RESULT 3
US-09-879-461-3
; Sequence 3, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; STREET: Swedeland Rd.
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64..483
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-879-461-3

Query Match 86.3%; Score 313.4; DB 10; Length 483;
Best Local Similarity 91.5%; Pred. No. 2e-97;
Matches 332; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 CAGGTTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGGCCCTCCAGACCCCTCAGTCTG 60
Db 121 CAGGTTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGGCCCTCCAGACCCCTCAGTCTG 180
Qy 61 ACTTGTCTTTCTCTGGTCTTCACTGAGCACTTCTGGTATGGGTGAGCTGGATTGGA 120
Db 181 ACTTGTCTTTCTCTGGTCTTCACTGAGCACTTCTGGTATGGGTGAGCTGGATTGGA 240
Qy 121 CAGCCTTCAGAAAGGCTCTGGATGGCTGGACACATTTACTGGGATGATGACAGCGC 180
Db 241 CAGCCTTCAGAAAGGCTCTGGATGGCTGGACACATTTACTGGGATGATGACAGCGC 300
```



Db 178 CAGCCTTCAGGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGATGATGACAAGCGC 237  
Qy 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCCAGGATACCTCCAGCAACAGGTA 240  
Db 238 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCCAGGATACCTCCAGCAACAGGTA 297  
Qy 241 TTCTCTCAAGATCACCAAGTGTGGACACTCGAGATCTGCCACATATCTACTGTCTCGAAGG 300  
Db 298 TTCTCTCAAGATCACCAAGTGTGGACCTCGAGATCTGCCACATATCTACTGTCTCGAAGG 357  
Qy 301 GTC-----TCTCTAAGTCTATGCTATGAGTACTGGGGTCAAGGAACCTCAGTCAAC 354  
Db 358 CCATTACTCCGGTACTAGTCGATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAAC 417  
Qy 355 GTCTCTCTCA 363  
Db 418 GTCTCTCTCA 426

## RESULT 6

US-09-995-529-11

; Sequence 11, Application US/09995529

; Publication No. US2003009655A1

; GENERAL INFORMATION:

; APPLICANT: Watkins, Jeffrey D.

; APPLICANT: Huse, William D.

; APPLICANT: Tang, Ying

; TITLE OF INVENTION: Humanized Collagen Antibodies and

; TITLE OF INVENTION: Related Methods

; FILE REFERENCE: P-IX 4976

; CURRENT APPLICATION NUMBER: US/09/995,529

; CURRENT FILING DATE: 2001-11-26

; NUMBER OF SEQ ID NOS: 358

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 369

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(369)

; US-09-995-529-11

Query Match 82.4%; Score 299; DB 11; Length 369;

Best Local Similarity 50.2%; Pred. No. 1.7e-92;

Matches 333; Conservative 0; Mismatches 30; Indels 6; Gaps 1;

Qy 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
Db 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
Qy 61 ACTTGTCTTTCTCTGGGTTTTCACCTGAGCATTCTGGTATGGGTGAGCTGGATTGGA 120  
Db 61 ACTTGTCTTTCTCTGGGTTTTCACCTGAGCATTCTGGTATGGGTGAGCTGGATTGCT 120  
Qy 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC 180  
Db 121 CAGCCTTCAGAGAGGCTCTAGAGTGGCTGGCACACATTTGTGGATGACATAAGTAC 180

Qy 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCCAGGATACCTCCAGCAACAGGTA 240  
Db 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCCAGGATACCTCCAGCAACAGGTA 240  
Qy 241 TTCTCTCAAGATCACCAAGTGTGGACACTCGAGATCTGCCACATATCTACTGTCTCGAAG 300  
Db 241 TTCTCTCAAGATCACCAAGTGTGGACACTCGAGATCTGCCACATATCTACTGTCTCGAAG 300  
Qy 301 G-----TCTCTCTAAGTCTATGCTATGAGTACTGGGGTCAAGGAACCTCAGTCAAC 354  
Db 301 GCTAACTATGTAACCCCTACTATGCTATGAGTACTGGGGTCAAGGAACCTCAGTCAAC 360  
Qy 355 GTCTCTCTCA 363

Db 361 GTCTCTCTCA 369

## RESULT 7

US-09-881-823-7

; Sequence 7, Application US/09881823

; Patent No. US20020068066A1

; GENERAL INFORMATION:

; APPLICANT: SHI, WENYUAN

; APPLICANT: ANDERSON, MAXWELL

; APPLICANT: MORRISON, SHERIE

; APPLICANT: TRINH, RYAN

; APPLICANT: WIMS, LETITIA

; APPLICANT: CHEN, LI

; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries

; FILE REFERENCE: 22851-032

; CURRENT APPLICATION NUMBER: US/09/881,823

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: US 07/378,577

; PRIOR FILING DATE: 1999-08-20

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 465

; TYPE: DNA

; ORGANISM: Murine

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (13)...(441)

; US-09-881-823-7

Query Match 78.3%; Score 284.4; DB 9; Length 465;

Best Local Similarity 88.0%; Pred. No. 1.9e-87;

Matches 322; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

Qy 1 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 60  
Db 70 CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCAGACCCCTCAGTCTG 129  
Qy 61 ACTTGTCTTTCTCTGGGTTTTCACCTGAGCATTCTGGTATGGGTGAGCTGGATTGGA 120  
Db 130 ACTTGTCTTTCTCTGGGTTTTCACCTGAGAACTTATGTTATAGGATAGGCTGGATTCTG 189  
Qy 121 CAGCCTTCAGAAAGGCTCTGGAGTGGCTGGCACACATTTACTGGGATGATGACAAGCGC 180  
Db 190 CAGCCTTCAGAGAGGCTCTGGAGTGGCTGGCACACATTTGTGGATGATGATATAGTAC 249  
Qy 181 TATAACCCATCCCTGAAGAGCGGCTTCAATCTCCAGGATACCTCCAGCAACAGGTA 240  
Db 250 TATAACACAGTCTCTGAAAGAGCGGCTTCAATCTCCAGGATACCTCCAGCAACAGGTA 309  
Qy 241 TTCTCTCAAGATCACCAAGTGTGGACACTCGAGATCTGCCACATATCTACTGTCTCGAAG 300  
Db 310 TTCTCTCAAGATCGCCAGTGTGGACACTCGAGATCTGCCACATATCTACTGTCTCGGGA 369  
Qy 301 GTCTCTCTAACTGGCT---ATGCTATGAGTACTCTGGGGTCAAGGAACCTCAGTCAACGTC 357  
Db 370 GAGGGGGCTCGGGTACGATGTTATGACTACTGGGGTCAAGGAATCTCAGTCAACGTC 429  
Qy 358 TCCTCA 363  
Db 430 TCCTCA 435

## RESULT 8

US-10-323-903-4

; Sequence 4, Application US/10323903

; Publication No. US20030228322A1

; GENERAL INFORMATION:

; APPLICANT: FISCHER, GERALD WALTER

; APPLICANT: SCHUMAN, RICHARD F.

; APPLICANT: MOND, JAMES JACOB

APPLICANT: KOKAI-KUN, JOHN FITZGERALD  
APPLICANT: POSTER, SIMON  
APPLICANT: STINSON, JEFFREY R.  
TITLE OF INVENTION: MULTIFUNCTIONAL MONOCLONAL ANTIBODIES DIRECTED TO  
FILE REFERENCE: 07787.0059  
CURRENT APPLICATION NUMBER: US/10/323,903  
CURRENT FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: 60/343,444  
PRIOR FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 09/097,055  
PRIOR FILING DATE: 1998-06-15  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 4  
LENGTH: 357  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(357)  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding  
M130 heavy chain antibody  
US-10-323-903-4

Query Match 74.6%; Score 270.8; DB 12; Length 357;  
Best Local Similarity 94.3%; Pred. No. 8.5e-83;  
Matches 281; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
QY 61 ACTGTTCTTTCTCTGGGTTTTCACGTAGCAGCATCTCTGGTATGGGTGAGCTGGATTGGA 120  
DB 61 ACTGTTCTTTCTCTGGGTTTTCACGTAGCAGCATCTCTGGTATGGGTGAGCTGGATTGCT 120  
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGGACACATTTACTGGATCATGACAGCGC 180  
DB 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGGACACATTTACTGGATCATGACAGCGC 180  
QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240  
DB 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240  
QY 241 TTCTCAAGATCACCACTGAGTGGGACTGCGATACCTGCGACATCTACTGTGCTCGAA 298  
DB 241 TTCTCAAGATCACCACTGAGTGGGACTGCGATACCTGCGACATCTACTGTGCTCGAA 298

RESULT 9  
US-09-764-304-1  
Sequence 1, Application US/09764304  
Patent No. US2002026036A1  
GENERAL INFORMATION:  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: HASEGAWA, MAMORU  
APPLICANT: MIYAJI, HIROMASA  
APPLICANT: KUWANA, YOSHIHISA  
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
FILE REFERENCE: 249-101  
CURRENT APPLICATION NUMBER: US/09/764,304  
CURRENT FILING DATE: 2001-01-19  
EARLIER APPLICATION NUMBER: 09/225,322  
EARLIER FILING DATE: 1999-01-05  
EARLIER APPLICATION NUMBER: US 08/454,680  
EARLIER FILING DATE: 1995-05-31  
EARLIER APPLICATION NUMBER: US 08/408,133  
EARLIER FILING DATE: 1995-03-21  
EARLIER APPLICATION NUMBER: US 08/292,178  
EARLIER FILING DATE: 1994-08-17

EARLIER APPLICATION NUMBER: US07/947,674  
EARLIER FILING DATE: 1992-09-17  
EARLIER APPLICATION NUMBER: JP 3-238375  
EARLIER FILING DATE: 1991-09-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 812  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Rat Hybridoma  
FEATURE:  
NAME/KEY: TATA signal  
LOCATION: (256)..(262)  
NAME/KEY: sig\_peptide  
LOCATION: (300)..(440)  
NAME/KEY: CDS  
LOCATION: (300)..(344)  
NAME/KEY: CDS  
LOCATION: (429)..(806)  
NAME/KEY: mat\_peptide  
LOCATION: (300)..(806)  
NAME/KEY: intron  
LOCATION: (345)..(428)  
US-09-764-304-1

Query Match 69.1%; Score 250.8; DB 9; Length 812;  
Best Local Similarity 82.2%; Pred. No. 8.8e-76;  
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;  
QY 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 441 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 500  
QY 61 ACTGTTCTTTCTCTGGGTTTTCACGTAGCAGCATCTCTGGTATGGGTGAGCTGGATTGGA 120  
DB 501 ACTGTTCTTTCTCTGGGTTTTCACGTAGCAGCATCTCTGGTATGGGTGAGCTGGATTGCT 560  
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180  
DB 561 CAGGTTCTTCAGGAAGGCTCTGGAGTGGCTGGGACACATTTGGTGGAGTGTGCTAAGTAC 620  
QY 181 TATAACCCATCCCTGAAGAGCCGGCTTACAATCTCAAGGATACCTCCAGCAACCCAGGTA 240  
DB 621 TACATCCATCTCTGAAGAACCCGCTCACAATCTCCAGGACACCTCCACACACCAAGCA 680  
QY 241 TTCTCAAGATCACCACTGAGTGGGACTGCGATACCTGCGACATCTACTGTGCTCGAAG 300  
DB 681 TTCTCAAGATCACCACTGAGTGGGACTGCGATACCTGCGACATCTACTGTGCTCGAAG 740  
QY 301 GTCTCTTAAGTGGCTATGCTA--TGGACTCTGGGGTCAAGGAACCTCAGTCACCGTC 357  
DB 741 GGGCTAGGAGGTATAGTGGCTTTGATTTCTGGGGCCACCGAGTCTGCTCAGTC 800  
QY 358 TCCTCA 363  
DB 801 TCCTCA 806

RESULT 10  
US-10-166-626-1  
Sequence 1, Application US/10166626  
Publication No. US20030166876A1  
GENERAL INFORMATION:  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: HASEGAWA, MAMORU  
APPLICANT: MIYAJI, HIROMASA  
APPLICANT: KUWANA, YOSHIHISA  
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
FILE REFERENCE: 249-101  
CURRENT APPLICATION NUMBER: US/10/166,626



CURRENT FILING DATE: 2002-06-12  
PRIOR APPLICATION NUMBER: US/09/225,322B  
PRIOR FILING DATE: 1999-01-05  
PRIOR APPLICATION NUMBER: US 08/454,680  
PRIOR FILING DATE: 1995-05-31  
PRIOR APPLICATION NUMBER: US 08/408,133  
PRIOR FILING DATE: 1995-03-21  
PRIOR APPLICATION NUMBER: US 08/292,178  
PRIOR FILING DATE: 1994-08-17  
PRIOR APPLICATION NUMBER: US07/947,674  
PRIOR FILING DATE: 1992-09-17  
PRIOR APPLICATION NUMBER: JP 3-238375  
PRIOR FILING DATE: 1991-09-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 1  
LENGTH: 812  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Rat Hybridoma  
NAME/KEY: TATA signal  
LOCATION: (256)..(262)  
FEATURE:  
NAME/KEY: sig peptide  
LOCATION: (300)..(440)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (300)..(344)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (429)..(806)  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: (300)..(806)  
FEATURE:  
NAME/KEY: intron  
LOCATION: (346)..(428)  
US-10-166-626-1

Query Match 69.1%; Score 250.8; DB 13; Length 812;  
Best Local Similarity 82.2%; Pred. No. 8.8e-76;  
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;  
QY 1 CAGGTTACTCTGAAGAGTCTGSCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 441 CAGGTTACTCTGAAGAAATCTGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 500  
QY 61 ACTTGTTCTTTCTCTGGTTTTCAGTACGACCTCTGGTATGGTGTGAGTGGATTGGA 120  
DB 501 ACTTGCTCTTTCTCTGGTTTTCAGTACGACCTCTGGTATGGTGTGAGTGGATTGCGT 560  
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTACTGGATGATGACAGCGC 180  
DB 561 CAGTCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTACTGGATGATGACAGCGC 620  
QY 181 TATAACCCATCCCTGGAAGACCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 240  
DB 621 TACAATCCATCTCTGAAACACCGGCTCACAATCTCAAGGATACCTCCAGCAACAGGTA 680  
QY 241 TTCTCTCAAGATCACCAGTGTGGACACTTCGAGATACCTCCAGATACCTCCAGCAACAGGTA 300  
DB 681 TTCTCTCAAGATCACCAGTGTGGACACTTCGAGATACCTCCAGATACCTCCAGCAACAGGTA 740  
QY 301 GTCTCTCAAGTGTGGACACTTCGAGATACCTCCAGATACCTCCAGCAACAGGTA 357  
DB 741 GGGGTACGGAGGATAGTGAAGCTTTGATTTACTGGGCGCACGGATCATGTTGATGATG 800  
QY 358 TCCTCA 363  
DB 801 TCCTCA 806

RESULT 11  
US-10-195-752-16  
Sequence 16, Application US/10195752  
Publication No. US2003007276A1  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
KOIKE, MASAMICHI  
SHITARA, KENYA  
HANAI, NOBUO  
KUWANA, YOSHIHISA  
HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHUYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/195,752  
FILING DATE: 16-Jul-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/393,385B  
FILING DATE: 27-JUN-96  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 812 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: HYBRIDOMA KM50  
FEATURE:  
NAME/KEY: TATA signal  
LOCATION: 261..267  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-10-195-752-16

Query Match 69.1%; Score 250.8; DB 15; Length 812;  
Best Local Similarity 82.2%; Pred. No. 8.8e-76;  
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;  
QY 1 CAGGTTACTCTGAAGAGTCTGSCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 60  
DB 441 CAGGTTACTCTGAAGAAATCTGCCCTGGGATATTCAGCCCTCCAGACCCCTCAGTCTG 500  
QY 61 ACTTGTTCTTTCTCTGGTTTTCAGTACGACCTCTGGTATGGTGTGAGTGGATTGGA 120  
DB 501 ACTTGCTCTTTCTCTGGTTTTCAGTACGACCTCTGGTATGGTGTGAGTGGATTGCGT 560  
QY 121 CAGCCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTACTGGATGATGACAGCGC 180  
DB 561 CAGTCTTCAGGAAGGCTCTGGAGTGGCTGGCACATTTACTGGATGATGACAGCGC 620  
QY 181 TATAACCCATCCCTGGAAGACCGGCTTACAATCTCAAGGATACCTCCAGCAACAGGTA 240  
DB 621 TACAATCCATCTCTGAAACACCGGCTCACAATCTCAAGGATACCTCCAGCAACAGGTA 680  
QY 241 TTCTCTCAAGATCACCAGTGTGGACACTTCGAGATACCTCCAGATACCTCCAGCAACAGG 300

Db 681 TTCCTCAAGATCAACCAATATGGACACTGCAGATACTGCCATATACTACTGTGTGGGAGA 740  
Qy 301 GTCTCTCTAACTGCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCAAGTC 357  
Db 741 GGGCTAGGAGGTATAGTACGCTTTGATTACTTGGGGCCACGAGTCAATGGTCACAGTC 800  
Qy 358 TCCTCA 363  
Db 801 TCCTCA 806

## RESULT 12

US-10-265-713-1  
; Sequence 1, Application US/10265713  
; Publication No. US20030095964A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: HASEGAWA, MAMORU  
; APPLICANT: MIYAJI, HIROMASA  
; APPLICANT: KUWANA, YOSHIIISA  
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY  
; FILE REFERENCE: 249-101  
; CURRENT APPLICATION NUMBER: US/10/265,713  
; CURRENT FILING DATE: 2002-10-08  
; PRIOR APPLICATION NUMBER: US/09/225,322  
; PRIOR FILING DATE: 1999-01-05  
; PRIOR APPLICATION NUMBER: US 08/454,680  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: US 08/408,133  
; PRIOR FILING DATE: 1995-03-21  
; PRIOR APPLICATION NUMBER: US 08/292,178  
; PRIOR FILING DATE: 1994-08-17  
; PRIOR APPLICATION NUMBER: US07/947,674  
; PRIOR FILING DATE: 1992-09-17  
; PRIOR APPLICATION NUMBER: JP 3-238375  
; PRIOR FILING DATE: 1991-09-18  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 812  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Rat Hybridoma  
; NAME/KEY: TATA signal  
; LOCATION: (256)..(262)  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (300)..(440)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (300)..(344)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (429)..(806)  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: (300)..(806)  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (346)..(428)  
US-10-265-713-1

Query Match 69.1%; Score 250.8; DB 15; Length 812;  
Best Local Similarity 82.2%; Pred. No. 8.9e-76;  
Matches 301; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60  
Db 441 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 500

Qy 61 ACTTGTTCTTCTCTGCGTCTTCTCACTGAGCACTTCTGTTATGGTGTGAGTGGATTCGA 120  
Db 501 ACTTGCTCTTCTCTGCGTCTTCTCACTGAGCACTTATGTTATGTTGTTGGTCTGGATTCTG 560  
Qy 121 CAGCCTTCAGGAAGGGTCTGGAGTGGCTGGCACACATTTTACTGGGATGATGACAAGCGC 180  
Db 561 CAGTCTTCAGGAAGGGTCTGGAGTGGCTGGCAACGTTTGGTGGAGTGTGCTAAGTAC 620  
Qy 181 TATRACCCATCCCTGAAGAGCGGCTTACATCTCCAGGATACCTCCAGAACCCAGTA 240  
Db 621 TCAATCCATCTCTGAANAACCGGCTCAATCTCCAAGGACACCTCCCAACCAAGCA 680  
Qy 241 TTCCTCAAGATCACCAGTGTGGACACTGCAGATACTGCCACATACTACTGTGCTCGAAG 300  
Db 681 TTCCTCAAGATCACCATAATGGACACTGCAGATACTGCCATATATACTACTGTGCTGGGAGA 740  
Qy 301 GTCTCTCTAACTGCTATGCTA---TGGACTACTGGGGTCAAGGAACCTCAGTCAAGTC 357  
Db 741 GGGCTACGGAGGTATAGTACGCTTTGATTACTTGGGGCCACGAGTCAATGGTCACAGTC 800  
Qy 358 TCCTCA 363  
Db 801 TCCTCA 806

## RESULT 13

US-10-255-478-50  
; Sequence 50, Application US/10255478  
; Publication No. US20030165498A1  
; GENERAL INFORMATION:  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Richard, Ruth A.  
; APPLICANT: Johnson, Kimberly S.  
; APPLICANT: Schlom, Jeffrey  
; APPLICANT: Kashmiri, Syed V.S.  
; APPLICANT: Shu, Liming  
; APPLICANT: Padlan, Eduardo A.  
; TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain  
; FILE REFERENCE: 37777E  
; CURRENT APPLICATION NUMBER: US/10/255,478  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: US/08/961,309  
; PRIOR FILING DATE: 1997-10-30  
; PRIOR APPLICATION NUMBER: US 60/030,173  
; PRIOR FILING DATE: 1996-10-31  
; PRIOR APPLICATION NUMBER: US 08/261,354  
; PRIOR FILING DATE: 1994-06-16  
; PRIOR APPLICATION NUMBER: US 07/964,536  
; PRIOR FILING DATE: 1992-10-20  
; PRIOR APPLICATION NUMBER: US 07/510,697  
; PRIOR FILING DATE: 1990-07-17  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: Microsoft Word 97 SR-2  
; SEQ ID NO 50  
; LENGTH: 423  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: B17X2 VH coding sequence  
; LOCATION: 7..423  
; OTHER INFORMATION: DNA encoding the heavy chain variable region of the anti-N-  
; OTHER INFORMATION: acetylglucosamine antibody, B17X2  
US-10-255-478-50

Query Match 52.7%; Score 191.4; DB 13; Length 423;  
Best Local Similarity 72.2%; Pred. No. 2e-55;  
Matches 262; Conservative 0; Mismatches 92; Indels 9; Gaps 1;

Qy 1 CAGGTTACTCTGAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGACCCCTCAGTCTG 60  
Db 64 CAGATCACCTTGAGGAGTCTGTCTTACNCTGGTGAACCCACACAGACCTTCAGCTG 123

QY 61 ACTTGTTCTTCTCTGGGTTTCACTGAGCACTCTGGTATGGGTGAGCTGGATTGGA 120  
|||  
Db 124 ACTGACCTTCTCTGGGTTTCACTGAGCACTCATGGAGTGGGTGTGGCTGGATCCGT 183  
|||  
QY 121 CAGCCTTCAGGAAAGGTTCTGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180  
|||  
Db 184 NNNNNCCAGGAAAGCCCTGGAGTGGCTTGCACTCAITTTATTGGGATGATGAAGCGC 243  
|||  
QY 181 TATAACCCATCCCTGGAAGAGCGGCTTCAATCTCCAAGGATACCTCCAGCAACAGGTA 240  
|||  
Db 244 TACAGCCCATCTCTGAAGAGAGGCTCACATCAACCAAGGACACTCCAAACACAGGTG 303  
|||  
QY 241 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGACATATCTATGCTCGAAGG 300  
|||  
Db 304 ATCCTTACAATGACCAACATGAGCCCTGTGGACACAGCCACATATTTATGTGCACACGGG 363  
|||  
QY 301 GTCTCTTAACCTGCTATGCTATGGAAGTCTGAGTCTGGGTCTGAGGACCTCACTGACCTCTCC 360  
|||  
Db 364 CT-----GCCATCTATGTTAAGAACTGGGGCCAAAGGACACAGGTCAACCTCTCC 414  
|||  
QY 361 TCA 363  
|||  
Db 415 TCA 417

## RESULT 14

US-10-072-301-22  
; Sequence 22, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCES: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 22  
; LENGTH: 759  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.24  
US-10-072-301-22

Query Match 50.4%; Score 183; DB 13; Length 759;  
Best Local Similarity 76.3%; Pred. No. 1.9e-52;  
Matches 225; Conservative 0; Mismatches 70; Indels 0; Gaps 0;  
QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGAGCCCTCAGTCTG 60  
|||  
Db 1 CAGGTACCTTGAAGGAGTCTGGTCTTACGCTGGTGAACCCACACAGACCCCTCAGCTG 60  
|||  
QY 61 ACTTGTTCTTCTCTGGGTTTCACTGAGCACTCTGGTATGGGTGAGCTGGATTGGA 120  
|||  
Db 61 ACCTGACCTTCTCTGGGTTTCACTCAGAACTACTGGAGAGGTTGGGCTGGTCCGT 120  
|||  
QY 121 CAGCCTTCAGGAAAGGTTCTGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180  
|||  
Db 121 CAGCCCCCAGGAAAGGCCCTTGAATGGCTTGCACTCAITTTATTGGGATGATGAAGCGC 180  
|||  
QY 181 TATAACCCATCCCTGGAAGAGCGGCTTACAATCTCCAAGGATACCTCCAGCAACAGGTA 240  
|||  
Db 181 TACAGCCCATCTCTGAAGAGAGGCTCACCATCACCAGGACACCTCCCAAAAGAGAGGTG 240  
|||  
QY 241 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGCCACATFACCTACTGTGCTC 295  
|||  
Db 241 GTCTTACAATGACCAACGTTGGAGCCGAGCGGACAGACCCACTTATTACTGTACAC 295  
|||

RESULT 15  
US-10-072-301-30  
; Sequence 30, Application US/10072301  
; Publication No. US20030152913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hua, Shao-bing  
; APPLICANT: Pauling, Michelle H.  
; APPLICANT: Zhu, Li  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF  
; FILE REFERENCES: 25636-718  
; CURRENT APPLICATION NUMBER: US/10/072,301  
; CURRENT FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 30  
; LENGTH: 759  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Clone 15.150.24 Variant  
US-10-072-301-30

Query Match 50.4%; Score 183; DB 13; Length 759;  
Best Local Similarity 76.3%; Pred. No. 1.9e-52;  
Matches 225; Conservative 0; Mismatches 70; Indels 0; Gaps 0;  
QY 1 CAGGTACTCTGAAAGAGTCTGGCCCTGGGATATTGAGCCCTCCAGAGCCCTCAGTCTG 60  
|||  
Db 1 CAGGTACCTTGAAGGAGTCTGGTCTTACGCTGGTGAACCCACACAGACCCCTCAGCTG 60  
|||  
QY 61 ACTTGTTCTTCTCTGGGTTTCACTGAGCACTCTGGTATGGGTGAGCTGGATTGGA 120  
|||  
Db 61 ACCTGACCTTCTCTGGGTTTCACTCAGAACTACTGGAGAGGTTGGGCTGGTCCGT 120  
|||  
QY 121 CAGCCTTCAGGAAAGGTTCTGAGTGGCTGGGACACATTTACTGGGATGATGACAGCGC 180  
|||  
Db 121 CAGCCCCCAGGAAAGGCCCTTGAATGGCTTGCACTCAITTTATTGGGATGATGAAGCGC 180  
|||  
QY 181 TATAACCCATCCCTGGAAGAGCGGCTTACAATCTCCAAGGATACCTCCAGCAACAGGTA 240  
|||  
Db 181 TACAGCCCATCTCTGAAGAGAGGCTCACCATCACCAGGACACCTCCCAAAAGAGAGGTG 240  
|||  
QY 241 TTCTCAAGATCACCAAGTGTGGACACTCGAGATACCTGCCACATFACCTACTGTGCTC 295  
|||  
Db 241 GTCTTACAATGACCAACGTTGGAGCCGAGCGGACAGACCCACTTATTACTGTACAC 295  
|||

Search completed: January 14, 2004, 19:01:59  
Job time : 218.81 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 17:47:02 ; Search time 37.1905 Seconds  
(without alignments)  
516.420 Million cell updates/sec

Title: US-09-759-112a-7

Perfect score: 633

Sequence: 1 QVTLKESGPCLLPQSOTLSL.....SLTAYMDYWGQTSVTWS 121

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	100.0	121	AA018528	Murine Mab 1F7 hea
2	569	89.9	140	AA018528	Mouse Mab 3B9 heav
3	569	89.9	140	AA018528	Heavy chain variab
4	569	89.9	140	AA018528	Heavy chain sequen
5	569	89.9	141	AA018528	Chimeric antibody
6	569	89.9	141	AA018528	Heavy chain variab
7	569	89.9	141	AA018528	Chimeric 3B9 monoc
8	567.5	89.7	246	AA018528	IL-6 binding inhib
9	551	87.0	142	ABG76934	Mouse 10D5 VH prot

10	545.5	86.3	122	15	AA018528
11	522.5	82.5	120	17	AA018528
12	522.5	82.5	139	16	AA018528
13	521.5	82.4	139	16	AA018528
14	520	82.1	121	23	ABG76934
15	516	81.5	121	20	AA018528
16	516	81.5	259	21	AA018528
17	516	81.5	259	22	AA018528
18	514	81.2	123	21	AA018528
19	509	80.4	470	21	AA018528
20	506.5	80.0	120	17	AA018528
21	506.5	80.0	120	23	ABG76934
22	506.5	80.0	143	23	ABG76934
23	505.5	79.9	143	15	AA018528
24	502	79.3	141	16	AA018528
25	502	79.3	141	20	AA018528
26	502	79.3	141	20	AA018528
27	500	79.0	121	20	AA018528
28	500	79.0	121	20	AA018528
29	494	78.0	123	24	ABP58287
30	494	78.0	453	24	ABP58287
31	494	78.0	472	24	ABP58287
32	476	75.2	123	24	ABP58287
33	470.5	74.3	141	14	AA018528
34	470.5	74.3	141	15	AA018528
35	470.5	74.3	141	15	AA018528
36	470.5	74.3	141	15	AA018528
37	468.5	74.0	120	22	AA018528
38	468.5	74.0	120	22	AA018528
39	468.5	74.0	450	23	ABP56542
40	468.5	74.0	450	24	ABU9445
41	467.5	73.9	120	23	ABG31432
42	466.5	73.7	120	17	AA018528
43	466.5	73.7	120	22	AA018528
44	466.5	73.7	120	22	AA018528
45	466.5	73.7	120	22	AA018528

#### ALIGNMENTS

#### RESULT 1

AA018528  
ID AA018528 standard; Protein; 121 AA.

AC AA018528;

DT 11-OCT-2002 (first entry)

DE Murine Mab 1F7 heavy chain.

KW Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;  
KW complementarity determining region; framework-determining region;  
KW FR; heavy chain; light chain; HIV infection.

OS Mus sp.

PN WO200255668-A2.

PD 18-JUL-2002.

PF 11-JAN-2002; 2002WO-US00927.

PR 11-JAN-2001; 2001US-0759112.

PA (IMMP-) IMMOPHERON INC.

PI Muller S, Kohler H;

DR WPI; 2002-590668/63.

XX N-PSDB; AAL48652.

PT New polynucleotide encoding a complementarity- or framework-determining

PT region of an anti-idiotypic antibody that binds to human or primate  
 PT anti-human immunodeficiency virus (HIV) antibodies, for use in  
 PT vaccines against HIV

XX Disclosure; Page 18-19; 27pp; English.

XX The present invention relates to coding sequences of the murine IF7  
 CC anti-idiotypic antibody complementarity-determining region (CDR) or  
 CC framework-determining region (FR). The antibody binds to human or primate  
 CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the  
 CC treatment of HIV infection. The present sequence is the IF7 heavy chain.

XX Sequence 121 AA;

Query Match 100.0%; Score 633; DB 23; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 7,3e-55;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVTLKESGPGIQLPSQTLTLTSCFSFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60  
 DB 1 QVTLKESGPGIQLPSQTLTLTSCFSFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60  
 QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGSVTVS 120  
 DB 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGSVTVS 120

QY 121 S 121

DB 121 S 121

#### RESULT 2

ID AAR70190 standard; Protein; 140 AA.

XX AAR70190;

XX 25-MAR-2003 (updated)

DT 20-SEP-1995 (first entry)

DE Mouse MAb 3B9 heavy chain.

XX Chimeric antibody; humanized antibody; antibody engineering;  
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.

XX Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig\_peptide

FT Region 50..56

FT /label= CDR

FT /note= "complementarity determining region"

FT 71..86

FT /label= CDR

FT /note= "complementarity determining region"

FT 119..129

FT /label= CDR

FT /note= "complementarity determining region"

XX WO9507301-A1.

XX 16-MAR-1995.

XX 07-SEP-1994; 94WO-US10308.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

PI WPI; 1999-429500/36.

XX WPI; 1995-123387/16.  
 DR N-PSDB; AAQ83491.

XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IGE-mediated allergic conditions  
 PS Disclosure; Fig.2; 97pp; English.

CC Spleen cells from mice immunized with human IL-4 were used to prepare  
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
 CC chains were cloned into pGEM7f+ and transformed into E. coli  
 CC DH5-alpha. The clones were sequenced (AAQ83490-91), and used for  
 CC antibody engineering.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 140 AA;

Query Match 89.9%; Score 569; DB 16; Length 140;  
 Best Local Similarity 90.1%; Pred. No. 1.8e-48;  
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGIQLPSQTLTLTSCFSFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60  
 DB 20 QVTLKESGPGIQLPSQTLTLTSCFSFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 79

QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGSVTVS 120

DB 80 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGSVTVS 139

QY 121 S 121

DB 140 S 140

#### RESULT 3

AA23768

ID AA23768 standard; Protein; 140 AA.

XX AA23768;

XX 13-SEP-1999 (first entry)

XX Heavy chain variable region of murine IL-4 antibody 3B9.

XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;  
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;  
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;  
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;  
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;  
 KW allergy.

XX Mus sp.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-429500/36.

DR N-PSDB; AAX85885.  
 XX New DNA molecules encoding recombinant antibodies useful for  
 PT treating IL4-mediated conditions  
 XX  
 PS Example 3; Fig 2; 50pp; English.  
 XX  
 CC The present sequence represents the heavy chain variable region of  
 CC murine interleukin-4 (IL-4) antibody 3B9. The sequences are used  
 CC in the production of chimeric and humanised IL-4 monoclonal antibodies.  
 CC The antibodies of the invention are used in therapeutic and  
 CC pharmaceutical compositions for treating IL-4 mediated and  
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,  
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,  
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.  
 CC They are also useful in the diagnosis of an allergy or condition  
 CC associated with excess IL-4 production through the measurement e.g. by  
 CC ELISA of circulating endogenous IL-4 levels in humans.  
 XX  
 SQ Sequence 140 AA;  
 Query Match 89.9%; Score 569; DB 20; Length 140;  
 Best Local Similarity 90.1%; Pred. No. 1.8e-48;  
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 QVTLKESGPGILQPSQTLSTLCSPGSLTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60  
 DB 20 QVTLKESGPGILQPSQTLSTLCSPGSLTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 79  
 QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120  
 DB 80 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 139  
 QY 121 S 121  
 DB 140 S 140  
 RESULT 4  
 AAY18121  
 ID AAY18121 standard; Protein; 140 AA.  
 XX AC AAY18121;  
 XX 11-AUG-1999 (first entry)  
 XX Heavy chain sequence for murine 3B9 antibody.  
 DE Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;  
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;  
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;  
 KW autoimmune disease; graft versus host disease.  
 XX OS Mus sp.  
 XX US5914110-A.  
 XX 22-JUN-1999.  
 XX 07-JUN-1995; 95US-0483636.  
 XX 07-JUN-1995; 95US-0483636.  
 XX 07-SEP-1993; 93US-0117366.  
 XX 14-OCT-1993; 93US-0136783.  
 XX 07-SEP-1994; 94WO-US10308.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX Gross MS, Holmes SD, Sylvester DR;  
 XX WPI; 1999-370482/31.  
 XX N-PSDB; AAX79520.  
 XX  
 XX Recombinant IL4 antibodies  
 XX Claim 24; Fig 2; 50pp; English.  
 XX  
 CC This sequence represents the heavy chain of the murine 3B9  
 CC antibody of the invention. The antibody is a chimeric or  
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of  
 CC immunoglobulin E (IGE) mediated diseases. The antibodies are useful for  
 CC the treatment of allergic disorders such as allergic rhinitis,  
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.  
 CC The antibodies are also useful for regulating B and T cell proliferation  
 CC and as such are useful in the treatment of autoimmune diseases and graft  
 CC versus host disease.  
 XX  
 SQ Sequence 140 AA;  
 Query Match 89.9%; Score 569; DB 20; Length 140;  
 Best Local Similarity 90.1%; Pred. No. 1.8e-48;  
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 QVTLKESGPGILQPSQTLSTLCSPGSLTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60  
 DB 20 QVTLKESGPGILQPSQTLSTLCSPGSLTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 79  
 QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120  
 DB 80 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 139  
 QY 121 S 121  
 DB 140 S 140  
 RESULT 5  
 AAR70191  
 ID AAR70191 standard; Protein; 141 AA.  
 XX AC AAR70191;  
 XX 25-MAR-2003 (updated)  
 XX 20-SEP-1995 (first entry)  
 XX Chimeric antibody 3B9 heavy chain.  
 DE Chimeric antibody; antibody engineering; monoclonal antibody;  
 KW MAB; interleukin-4; IL-4; allergy.  
 XX OS Homo sapiens; Mus sp.  
 XX Key Location/Qualifiers  
 FT Peptide  
 FT /label= Sig\_peptide  
 FT /label= CDR  
 FT /note= "complementarity determining region#" 72..87  
 FT /label= CDR  
 FT /note= "complementarity determining region" 120..130  
 FT /label= CDR  
 FT /note= "complementarity determining region" 120..130  
 PN WO9507301-A1.  
 XX 16-MAR-1995.  
 XX 07-SEP-1994; 94WO-US10308.  
 XX 07-SEP-1993; 93US-0117366.  
 XX 14-OCT-1993; 93US-0136783.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1995-123387/16.

DR N-PSDB; AAQ83492.

XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived from high affinity mAbs - useful in treatment of IL-4-mediated PT and IgE-mediated allergic conditions

XX Disclosure; Fig.3; 97pp; English.

XX A human/mouse chimeric antibody heavy chain variable region was constructed (given in AAR70191) that contained the mouse anti-human CC IL-4 MAB 3B9 variable region including 3 CDRs (AAR70199-200) and a CC human antibody signal peptide (AAR70193). The construct was used CC for humanised antibody production.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 141 AA;

SQ Query Match 89.9%; Score 569; DB 16; Length 141;

Best Local Similarity 90.1%; Pred. No. 1.8e-48;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILOPQSOTLSLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60

DB 21 QVTLKESGPGILOPQSOTLSLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 80

QY 61 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSTVTS 120

DB 81 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYYCARRVTFVYFVWVGAGITVTS 140

QY 121 S 121

DB 141 S 141

RESULT 6

AAAY23769

ID AAY23769 standard; Protein; 141 AA.

XX AC AAY23769;

DT 13-SEP-1999 (first entry)

XX Heavy chain variable region of murine/human chimeric antibody 3B9.

XX Heavy chain variable region; interleukin-4; IL-4; antibody 3B9;  
KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;  
KW Immunoglobulin E-mediated allergic reaction; allergic rhinitis;  
KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;  
KW rheumatoid arthritis; host-versus-graft disease; renal disease;  
KW allergy.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX US928904-A.

PD 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

PR 07-SEP-1993; 93US-0117366.

PR 14-OCT-1993; 93US-0136783.

PR 07-SEP-1994; 94WO-US10308.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-429500/36.

DR N-PSDB; AAX85886.

XX New DNA molecules encoding recombinant antibodies useful for PT treating IL4-mediated conditions

XX Example 3; Fig 3; 50pp; English.

XX The present sequence represents the heavy chain variable region of CC murine/human interleukin-4 (IL-4) chimeric antibody 3B9. The CC specification describes chimeric and humanised IL-4 monoclonal CC antibodies. The antibodies of the invention are used in therapeutic CC and pharmaceutical compositions for treating IL-4 mediated and CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, CC rheumatoid arthritis, host-versus-graft disease and renal disease. CC They are also useful in the diagnosis of an allergy or condition CC associated with excess IL-4 production through the measurement e.g. by CC ELISA of circulating endogenous IL-4 levels in humans.

SQ Sequence 141 AA;

Query Match 89.9%; Score 569; DB 20; Length 141;

Best Local Similarity 90.1%; Pred. No. 1.8e-48;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILOPQSOTLSLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60

DB 21 QVTLKESGPGILOPQSOTLSLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 80

QY 61 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSTVTS 120

DB 81 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYYCARRVTFVYFVWVGAGITVTS 140

QY 121 S 121

DB 141 S 141

RESULT 7

AAAY18125

ID AAY18125 standard; Protein; 141 AA.

XX AC AAY18125;

DT 11-AUG-1999 (first entry)

XX Chimeric 3B9 monoclonal antibody heavy chain.

XX Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;  
KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;  
KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;  
KW autoimmune disease; graft versus host disease.

XX Synthetic.

XX US5914110-A.

PD 22-JUN-1999.

XX 07-JUN-1995; 95US-0483636.

XX 07-JUN-1995; 95US-0483636.

PR 07-SEP-1993; 93US-0117366.

PR 14-OCT-1993; 93US-0136783.

PR 07-SEP-1994; 94WO-US10308.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-370482/31.  
 DR N-PSDB; AAX79542.  
 XX Recombinant IL4 antibodies  
 PS Example 5; Fig 3; 50pp; English.  
 XX This sequence represents the light chain of the chimeric  
 CC 3B9 antibody of the invention. The antibody is a chimeric or  
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of  
 CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for  
 CC the treatment of allergic disorders such as allergic rhinitis,  
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.  
 CC The antibodies are also useful for regulating B and T cell proliferation  
 CC and as such are useful in the treatment of autoimmune diseases and graft  
 CC versus host disease.  
 XX Sequence 141 AA;  
 SQ  
 Query Match 89.9%; Score 569; DB 20; Length 141;  
 Best Local Similarity 90.1%; Pred. No. 1.8e-48;  
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 QVTLKESGPGILOPQTLSLTCSFGSLSTSGVSWIRQPSGKGLEWLAHIYWDGDKR 60  
 Db 21 QVTLKESGPGILOPQTLSLTCSFGSLSTSGVSWIRQPSGKGLEWLAHIYWDGDKR 80  
 QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVDTTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120  
 Db 81 YNPSLKSLRLTISKDTSSNQVFLKITSVDTTRDTATYTCARRVTFYVYFDVWGAGITVTVS 140  
 QY 121 S 121  
 Db 141 S 141  
 RESULT 8  
 AARS8612  
 ID AARS8612 standard; Protein; 246 AA.  
 XX  
 AC AARS8612;  
 XX 25-MAR-2003 (updated)  
 DT 28-APR-1995 (first entry)  
 DE IL-6 binding inhibitor.  
 XX Human interleukin-6 binding inhibitor; IL-6; rheumatoid arthritis;  
 KW septic shock; multiple myeloma; ss.  
 XX Homo sapiens.  
 OS  
 XX EP617126-A2.  
 XX 28-SEP-1994.  
 XX 16-FEB-1994; 94EP-0102346.  
 XX 17-FEB-1993; 93JP-0028173.  
 XX (AJIN ) AJINOMOTO KK.  
 XX Hamuro J, Nakazawa H, Shimamura T;  
 PI WPI; 1994-295777/37.  
 DR N-PSDB; AAQ70612.  
 XX Polypeptide inhibiting binding of human interleukin-6 (IL-6) to  
 PT its receptor - useful for treating auto:immune disease induced  
 PT or aggravated by IL-6  
 XX Claim 5; Page 18; 26pp; English.

XX AAQ70612 codes for human interleukin-6 binding inhibitor, the  
 CC polypeptide described in AARS8612. This polypeptide inhibits the  
 CC binding of human IL-6 to its receptor, and can therefore be  
 CC useful in the treatment of a variety of autoimmune diseases;  
 CC specifically in the treatment of rheumatoid arthritis, septic  
 CC shock due to bacterial infection and multiple myeloma.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 246 AA;  
 SQ  
 Query Match 89.7%; Score 567.5; DB 15; Length 246;  
 Best Local Similarity 89.6%; Pred. No. 4.9e-48;  
 Matches 112; Conservative 3; Mismatches 5; Indels 5; Gaps 2;  
 QY 1 QVTLKESGPGILOPQTLSLTCSFGSLSTSGVSWIRQPSGKGLEWLAHIYWDGDKR 60  
 Db 123 QVTLKESGPGILOPQTLSLTCSFGSLSTSGVSWIRQPSGKGLEWLAHIYWDGDKR 182  
 QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVDTTRDTATYTCARRVSLTA----YAMDYWGQTS 116  
 Db 183 YNPSLKSLRLTISKDTSSNQVFLKITSVDTTRDTATYTCARR-SLYGNWGDYAMDYWGQTS 241  
 QY 117 VTSS 121  
 Db 242 VTSS 246  
 RESULT 9  
 ABG76934  
 ID ABG76934 standard; Protein; 142 AA.  
 XX  
 AC ABG76934;  
 XX 05-NOV-2002 (first entry)  
 DT Mouse 10D5 VH protein.  
 DE  
 XX Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;  
 KW variable region complementarity determining region; 3D6; 10D5;  
 KW variable framework region; amyloidogenic disease; Alzheimer's disease;  
 KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;  
 KW nototropic; neuroprotective; inhibitor of beta amyloid accumulation;  
 KW Abeta.  
 XX Mus musculus.  
 OS  
 XX WO200246237-A2.  
 PN 13-JUN-2002.  
 PD  
 PF 06-DEC-2001; 2001WO-US46587.  
 XX 06-DEC-2000; 2000US-251892P.  
 PR (NEUR-) NEURALAB LTD.  
 PA (AMHP) WYETH.  
 XX Basi G, Saldanha J, Yednock T;  
 PI WPI; 2002-519658/55.  
 DR N-PSDB; ABS59429.  
 XX Novel light/heavy chain of humanized immunoglobulin for treating  
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity  
 PT determining regions and variable framework region from human acceptor  
 PT immunoglobulin -  
 XX Claim 142; Figure 10; 171pp; English.  
 PS The present invention relates to new humanized immunoglobulin (Ig) light  
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity  
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,



CC and variable framework region from human acceptor Ig LC or HC sequence.  
 CC The invention is useful for preventing or treating an amyloidogenic  
 CC disease or Alzheimer's disease in a patient. The invention is also useful  
 CC for in vivo imaging amyloid deposits in a patient. The present amino  
 CC acid sequence represents a mouse J26/10D5 variable light (VL) chain or  
 CC variable heavy (VH) chain protein of the invention.

XX  
 SQ Sequence 142 AA;  
 Query Match 87.0%; Score 551; DB 23; Length 142;  
 Best Local Similarity 87.8%; Pred. NO. 1.1e-46;  
 Matches 108; Conservative 1; Mismatches 12; Indels 2; Gaps 1;  
 QY 1 QVTLKESGPGIILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60  
 DB 20 QATLKESGPGIILQSSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 79  
 QY 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYYCARR--VSLTAYAMDYWGQGTSTV 118  
 DB 80 YNPSLKSRLLTISKDTSRKQVFLKITSVDPADTATYYCVRRTPTVLVDAMDYWGQGTSTV 139  
 QY 119 VSS 121  
 DB 140 VSS 142

RESULT 10  
 AAR54101  
 ID AAR54101 standard; Protein; 122 AA.  
 XX  
 AC AAR54101;  
 XX  
 DT 08-FEB-1995 (first entry)  
 XX  
 DE Humanised MAb H-chain.  
 XX  
 KW Human; murine; heavy; light; chain; monoclonal; antibody;  
 KW complementarity determining region; CDR; IgG; kappa; IiIB; IiIM.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 31..37  
 FT /label= CDR1  
 FT Region 52..67  
 FT /label= CDR2  
 FT Region 100..111  
 FT /label= CDR3  
 XX  
 PN JP06141885-A.  
 XX  
 PD 24-MAY-1994.  
 XX  
 PF 05-NOV-1992; 92JP-0322476.  
 XX  
 PR 05-NOV-1992; 92JP-0322476.  
 XX  
 PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
 XX  
 DR WPI; 1994-205040/25.  
 DR N-PSDB; AAQ68709.  
 XX  
 PT Recombinant anti-HIV monoclonal antibody - capable of  
 PT neutralising strains which can not be neutralised by anti-IiIB  
 PT and IiIMN antibodies  
 XX  
 PS Disclosure; Page 13; 23pp; Japanese.  
 XX  
 CC The sequences given in AAR54101-02 represent the heavy and light chains  
 CC respectively of the humanised monoclonal antibody (MAb) of the  
 CC invention. The antibody has the ability to neutralise human  
 CC immunodeficiency virus. The antibody is classified as IgG kappa and

CC has the sequence RIGPCR or RVGPCR in the principal neutralising  
 CC domain. The antibody may be used to neutralise the clinically  
 CC separate strains which cannot be neutralised by the neutralising  
 CC antibodies against IiIB and IiIMN strains.

XX  
 SQ Sequence 122 AA;  
 Query Match 86.3%; Score 546.5; DB 15; Length 122;  
 Best Local Similarity 87.7%; Pred. NO. 2.5e-46;  
 Matches 107; Conservative 5; Mismatches 9; Indels 1; Gaps 1;  
 QY 1 QVTLKESGPGIILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60  
 DB 1 QVTLKESGPGIILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIYWDGDKH 60  
 QY 61 YNPSLKSRLLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSL-TAYAMDYWGQGTSTV 119  
 DB 61 YNPSLKSRLLTISEDTSNNQVFLKITTVDIADTATYYCARRVFGNSDFMDHWGQGTSTV 120  
 QY 120 SS 121  
 DB 121 SS 122

RESULT 11  
 AAR88109  
 ID AAR88109 standard; peptide; 120 AA.  
 XX  
 AC AAR88109;  
 XX  
 DT 25-JUL-1996 (first entry)  
 XX  
 DE Murine anti-Protein C MAb HPC-4 VH gamma mature peptide.  
 XX  
 KW Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
 KW zymogen; cleavage; mouse; humanised antibody; variable region;  
 KW light chain; inhibition; anticoagulant; coagulation; tumour.  
 XX  
 OS Mus musculus.  
 XX  
 PN W09534652-A1.  
 XX  
 PD 21-DEC-1995.  
 XX  
 PF 09-JUN-1995; 95WO-US07372.  
 XX  
 PR 10-JUN-1994; 94US-0259321.  
 XX  
 PA (OKLA-) OKLAHOMA MED RES FOUND.  
 XX  
 PI Esmon CT, Rezaie A;  
 XX  
 DR WPI; 1996-049681/05.  
 DR N-PSDB; AAT09300.  
 XX  
 PT Calcium-binding monoclonal antibody immunoreactive with Protein C -  
 PT inhibits Protein C anticoagulant activation by  
 PT thrombin-thrombomodulin, e.g. for treating tumours  
 XX  
 PS Claim 2; Page 29; 41pp; English.  
 XX  
 CC This is the amino acid sequence of the mature peptide from the murine  
 CC anti-protein C monoclonal antibody HPC-4 heavy chain variable region.  
 CC HPC-4 recognises the activation peptide region (AAR88106) of the heavy  
 CC chain of protein C, a vitamin K-dependent plasma protein zymogen.  
 CC Protein C is converted to activated protein C (APC) by cleavage between  
 CC the Arg-Leu amino acid contained within the activation peptide sequence.  
 CC HPC-4 prevents protein C activation to APC by binding to this region.  
 CC The DNA sequences encoding the variable regions of the heavy and light  
 CC chains of the antibody (AAT09299-302) were used to construct humanised  
 CC antibodies using the PCR primers AAT09303-9. The humanised antibodies  
 CC are useful as inhibitors of coagulation and can be used for the treatment  
 CC of tumours by inhibiting the anticoagulant activity of APC by preventing

CC conversion of protein C to APC.  
 XX Sequence 120 AA;  
 SQ Query Match 82.5%; Score 522.5; DB 17; Length 120;  
 Best Local Similarity 84.3%; Pred. No. 5.8e-44;  
 Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILOPQSQTLSLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60  
 DB 1 QVTLKESGPGILOPQSQTLSLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60  
 QY 61 YNPSLKSRLLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTVS 120  
 DB 61 YNPSLKSRLLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTVS 119

QY 121 S 121  
 DB 120 S 120

RESULT 12  
 AAR88107  
 ID AAR88107 standard; Protein; 139 AA.  
 XX AAR88107;  
 DT 25-JUL-1996 (first entry)  
 XX Murine anti-Protein C MAB HPC-4 VH gamma protein.  
 DE Epitope; activation; heavy chain; protein C; vitamin K; plasma protein;  
 KW zymogen; cleavage; mouse; humanised antibody; variable region;  
 KW light chain; inhibition; anticoagulant; coagulation; tumour.  
 XX Mus musculus.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /note= "signal peptide"  
 FT 20..139  
 FT /note= "mature peptide"  
 XX WO9534652-A1.  
 PN 21-DEC-1995.  
 PD 09-JUN-1995; 95WO-US07372.  
 XX 10-JUN-1994; 94US-0259321.  
 XX (OKLA-) OKLAHOMA MED RES FOUND.  
 XX Esmon CT, Rezaie A;  
 XX WPI; 1996-049681/05.  
 DR N-PSDB; AAT09299.  
 XX Calcium-binding monoclonal antibody immunoreactive with Protein C -  
 PT inhibits Protein C anticoagulant activation by  
 PT thrombin-thrombomodulin, e.g. for treating tumours  
 XX Claim 2; Page 29; 41pp; English.  
 XX This is the amino acid sequence of the heavy chain variable region from  
 CC the murine anti-protein C monoclonal antibody HPC-4 which recognises  
 CC the activation peptide region (AAR88106) of the heavy chain of protein  
 CC C, a vitamin K-dependent plasma protein zymogen. Protein C is converted  
 CC to activated protein C (APC) by cleavage between the Arg-Leu amino acid  
 CC contained within the activation peptide sequence. HPC-4 prevents  
 CC protein C activation to APC by binding to this region. The DNA sequences  
 CC encoding the variable regions of the heavy and light chains of the  
 CC antibody (AAT09299-302) were used to construct humanised antibodies using

CC the PCR primers AAT09303-9. The humanised antibodies are useful as  
 CC inhibitors of coagulation and can be used for the treatment of tumours by  
 CC inhibiting the anticoagulant activity of APC by preventing conversion of  
 CC protein C to APC.  
 XX Sequence 139 AA;  
 SQ Query Match 82.5%; Score 522.5; DB 17; Length 139;  
 Best Local Similarity 84.3%; Pred. No. 6.9e-44;  
 Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILOPQSQTLSLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60  
 DB 20 QVTLKESGPGILOPQSQTLSLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 79  
 QY 61 YNPSLKSRLLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTVS 120  
 DB 80 YNPSLKSRLLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTVS 138  
 QY 121 S 121  
 DB 139 S 139

RESULT 13  
 AAR67655  
 ID AAR67655 standard; Protein; 139 AA.  
 XX AAR67655;  
 AC 25-MAR-2003 (updated)  
 DT 21-AUG-1995 (first entry)  
 XX Mouse heavy chain variable region amino acid sequence.  
 DE Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;  
 KW interleukin; antibody; hybridoma; CDR; framework; constant region;  
 KW heavy chain; disorder; antigenicity.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /label= signal peptide  
 FT 20..139  
 FT /label= mature peptide  
 XX WO9428159-A1.  
 PN 08-DEC-1994.  
 PD 30-MAY-1994; 94WO-JPC00859.  
 XX 31-MAY-1993; 93JP-0129787.  
 PR (CHUS) CHUGAI SEIYAKU KK.  
 PA (CHUS) CHUGAI PHARM CO LTD.  
 XX Hirata Y, Sato K, Tsuchiya M;  
 XX WPI; 1995-022828/03.  
 DR N-PSDB; AAQ75889.  
 XX Antibody against IL-6 - useful for the therapy and treatment of  
 PT IL-6 related disorders.  
 XX Claim 10; Page 49; 82pp; Japanese.  
 XX The deduced amino acid sequence of the heavy chain variable region of  
 CC the mouse anti-human interleukin-6 (IL-6) antibody. The gene was  
 CC amplified by primers (AA075876-87) from cDNA derived from mRNA from  
 CC mouse SK2 hybridoma cells. The fragment was cloned into plasmid pUC19  
 CC to produce plasmid pUC-SK2-Vh. The inserted fragment is used to

CC generate constructs (see AAQ75914-7) encoding fragments of an antibody to  
 CC the human IL-6 comprising (a) a light chain with (i) a variable region  
 CC containing 3 complementarity determining regions (CDR) (AAR77201-3)  
 CC inserted into several framework regions (FR) (AAR77204-7) and (ii) a human  
 CC light chain constant region and (b) a heavy chain with (i) a variable  
 CC region containing 3 CDR (AAR77212-4) inserted into an FR (AAR77215-8) and  
 CC (ii) a human light chain constant region. The FR of the light chain may  
 CC be mouse derived (AAQ75888) or from the human antibody RE1. The heavy  
 CC chain FR may also be mouse derived (AAQ75889) or from the human antibody  
 CC DAW. The antibodies can be used in the treatment of IL-6 related  
 CC disorders. The antibodies are useful as they have low antigenicity due to  
 CC the use of human derived sequences and low antigenicity mouse derived  
 CC sequences.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 139 AA;  
 Query Match 82.4%; Score 521.5; DB 16; Length 139;  
 Best Local Similarity 83.7%; Pred. No. 8.7e-44;  
 Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;  
 QY 1 QVTLKESGPGIQLPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDKDKR 60  
 DB 20 QVTLKESGPGIQLPSQTLTLTCSFSGFSLSTSGMTVGWIRQPSGKGLWLAHIWWDKDY 79  
 QY 61 YNPPLKSLRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAY--AMDYWGQGTSTV 118  
 DB 80 YNPPLKSLRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAY--WEDYDEANDYWGQGTSTV 136  
 QY 119 VSS 121  
 DB 137 VSS 139

RESULT 14  
 ABG67188  
 ID ABG67188 standard; Protein; 121 AA.  
 AC ABG67188;  
 DT 24-SEP-2002 (first entry)  
 DE Human IgG1 antibody heavy chain variable region 15H4VH.  
 XX Hepatitis C virus vaccine; HCV; hypervariable region 1; HVR1;  
 KW envelope protein E2; antibody; helper T-lymphocyte; IgG1;  
 KW cytotoxic T-lymphocyte; HCV infection; virucide; heavy chain.  
 XX Homo sapiens.  
 OS  
 XX WO200245743-A2.  
 PN 13-JUN-2002.  
 PD 07-DEC-2001; 2001WO-GB05421.  
 PF 09-DEC-2000; 2000GB-0030102.  
 PR 18-DEC-2000; 2000GB-0030789.  
 XX (ALLA/) ALLAIN J.  
 PA Allain J, Li C, Piccolella E;  
 XX WPI; 2002-508540/54.  
 DR Hepatitis C virus (HCV) vaccines able to raise antibodies, helper T  
 XX lymphocytes and/or cytotoxic T lymphocytes able to bind to the  
 PT hypervariable 1 region of the infecting HCV strain -  
 XX Example 4; Fig 2; 52pp; English.  
 PS The present invention relates to a hepatitis C virus (HCV) vaccine  
 XX comprising different groups of peptides each group being capable of

CC raising, in an infected individual, an antibody able to bind to the  
 CC hypervariable 1 (HVR1) region of the envelope protein E2 of the  
 CC infecting HCV strain. The different groups of peptides are  
 CC administered sequentially to raise antibodies, helper T-lymphocytes,  
 CC and cytotoxic T-lymphocytes which are cross-reactive to the HVR1  
 CC region of the infecting HCV. The vaccines are useful for preventing  
 CC and treating chronic HCV infections. ABG67188-ABG67189 represent  
 CC variable regions of human IgG1 antibody heavy chain.

XX SQ Sequence 121 AA;  
 Query Match 82.1%; Score 520; DB 23; Length 121;  
 Best Local Similarity 85.2%; Pred. No. 1e-43;  
 Matches 104; Conservative 7; Mismatches 7; Indels 4; Gaps 3;  
 QY 1 QVTLKESGPGIQLPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHIY-WDDDK 59  
 DB 1 QVTLKESGPGIQLPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYPWDDDK 60  
 QY 60 RYNPLKSLRLTISKDTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGTSTV 119  
 DB 61 RYNPLKSLRLTISKDTSSNOVFLKITSVDTRDTATYYCAQIIT-TWFA--HWGQGLTIV 117  
 QY 120 SS 121  
 DB 118 SS 119

RESULT 15  
 AAY25396  
 ID AAY25396 standard; Protein; 121 AA.  
 AC AAY25396;  
 XX 07-SEP-1999 (first entry)  
 DT WO9932630 Seq ID 35.  
 DE Paraquat; antibody; light chain; herbicide; resistant; crop plant;  
 KW weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I;  
 KW free radical; lipid peroxidation; electron transport; photosystem II;  
 KW vacuole; cell surface; cytotoxic; sensitive.  
 XX Unidentified.  
 OS  
 XX WO9932630-A1.  
 PN 01-JUL-1999.  
 PD 15-DEC-1998; 98WO-GB03760.  
 PF 19-DEC-1997; 97GB-0026955.  
 PR (ZENE) ZENECA LTD.  
 PA Holt DC, Jones PG;  
 XX WPI; 1999-405173/34.  
 PT Herbicide binding proteins and related polynucleotides  
 XX Disclosure; Page 43-44; 60pp; English.

XX This invention describes a novel herbicide binding protein which can  
 CC confer herbicide resistance activity. Crop plants, such as soybean,  
 CC cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower,  
 CC potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas,  
 CC barley, oat, turf grass, forage grass, sugar cane, pea, field bean,  
 CC rice, pine, poplar, apple, grape, citrus or nut plants, transformed  
 CC with a herbicide binding protein gene are resistant to the herbicide.  
 CC Hence, weeds can be selectively controlled in a field of the transformed  
 CC crops. The plants are substantially resistant or tolerant to herbicides,  
 CC such as paraquat or diquat, that inhibit photosynthesis by accepting

Search completed: January 14, 2004, 19:11:24  
Job time : 40.1905 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 19:02:07 ; Search time 16.2381 Seconds  
(without alignments)  
716.612 Million cell updates/sec

Title: US-09-759-112A-7  
Perfect score: 633  
Sequence: 1 QVTLKESGPGILQPSQTLSL.....SLTAYAMYWGQGSTVTSS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	551.5	87.1	122	2 S11740	Ig heavy chain pre
2	543.5	85.9	143	2 PT0174	Ig heavy chain pre
3	491	77.6	107	2 A49442	Ig heavy chain V r
4	474.5	75.0	113	2 S26465	Ig heavy chain V r
5	472.5	74.6	116	2 S26328	Ig heavy chain V r
6	471	74.4	138	2 S31513	Ig heavy chain - h
7	460	72.7	121	2 S09959	Ig heavy chain V r
8	454.5	71.8	124	2 A49002	Ig heavy chain V r
9	448	70.8	103	2 B25913	Ig heavy chain pre
10	436	68.9	374	2 S69339	Ig heavy chain V r
11	419.5	66.3	120	1 GIHUCO	Ig heavy chain V-I
12	412	65.1	121	2 A36005	Ig heavy chain V r
13	410	64.8	119	2 S18555	Ig heavy chain V r
14	407	64.3	125	1 MHHUWC	Ig heavy chain V-I
15	402.5	63.6	147	1 G2HUCS	Ig heavy chain pre
16	395	62.4	121	1 G1HUHE	Ig heavy chain V r
17	390.5	61.7	122	2 S20809	Ig heavy chain V r
18	384.5	60.7	120	2 FL0087	Ig heavy chain V r
19	384	60.7	144	1 G2MS14	Ig heavy chain V r
20	383.5	60.6	118	2 S18556	Ig heavy chain pre
21	382	60.3	146	2 S09711	Ig heavy chain V r
22	379.5	60.0	117	2 S38563	Ig heavy chain V r
23	377	59.6	96	2 S26924	Ig heavy chain V r
24	376	59.4	140	2 I37782	Ig variable region
25	373.5	59.0	147	2 S13519	Ig heavy chain V r
26	373.5	59.0	122	2 A49049	Ig heavy chain V r
27	373.5	59.0	137	2 S31676	Ig heavy chain V r
28	372	58.8	155	2 S31511	Ig heavy chain - h
29	371	58.6	96	2 S26923	Ig heavy chain V r

30 371 58.6 109 2 PH1023 Ig heavy chain V r  
31 371 58.6 119 1 GIHUDW Ig heavy chain V-I  
32 371 58.6 140 2 S55028 Ig heavy chain V r  
33 370.5 58.5 130 2 S30534 Ig heavy chain V r  
34 370 58.5 155 2 S31512 Ig heavy chain - h  
35 369 58.3 130 2 S31690 Ig heavy chain V r  
36 368.5 58.2 139 2 A32456 Ig heavy chain pre  
37 368.5 58.2 141 2 S52446 Ig heavy chain V r  
38 368 58.1 117 2 S52446 gene C72-3A1 prote  
39 366 57.8 111 2 S26324 Ig heavy chain V r  
40 363 57.3 149 2 S30752 Ig heavy chain pre  
41 362 57.2 128 2 S31514 Ig heavy chain - h  
42 360.5 57.0 129 2 S44114 Ig heavy chain V r  
43 360 56.9 127 2 S19668 Ig heavy chain V r  
44 360 56.9 135 2 S78051 Ig heavy chain pre  
45 359.5 56.8 139 2 S31586 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S11740  
Ig heavy chain precursor V-D-J region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S11740  
R:Hayakawa, K.; Carmarck, C.E.; Hyman, R.; Hardy, R.R.  
submitted to the EMBL Data Library, May 1990  
A:Description: Natural autoantibodies to thymocytes: Origin, VH genes, fine specificity.  
A:Reference number: S11740  
A:Accession: S11740  
A:Molecule type: mRNA  
A:Residues: 1-122 <EMB>  
A:Cross-references: EMBL:X53097; NID:G52368; PIDN:CAA37261.1; PID:G762983  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:22-106/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 551.5; DB 2; Length 122;  
Best Local Similarity 91.4%; Pred. No. 3.4e-45;  
Matches 106; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSLTCSFGSLSTSGMGSWIRQPSGKGLWLAHYWDDDKR 60  
Db 8 QVTLKESGPGILQPSQTLSLTCSFGSLSTSGMGSWIRQPSGKGLWLAHYWDDDKR 67  
QY 61 YNPSLKRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMYWGQGSTS 116  
Db 68 YNPSLKRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMYWGQGSTS 122

RESULT 2

PT0174  
Ig heavy chain precursor V region (IdB5.7) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 16-Aug-1996  
C:Accession: PT0174  
R:Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.  
Mol. Immunol. 28, 505-515, 1991  
A:Title: Specificity and variable region cDNA sequence of an isogeneic monoclonal anti:  
A:Reference number: PT0174; MUID:91287738; PMID:1712074  
A:Accession: PT0174  
A:Molecule type: mRNA  
A:Residues: 1-143 <PER>  
A:Experimental source: strain BALB/c  
C:Comment: IdB5.7 is an antibody to anti-alpha (1-6) dextran.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 85.9%; Score 543.5; DB 2; Length 143;  
Best Local Similarity 85.7%; Pred. No. 2.3e-44;

Matches 108; Conservative 2; Mismatches 9; Indels 7; Gaps 2;

QY 1 QVTLKESGPILOPQSTLSLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
 Db 20 QVTLKESGPILOPQSTLSLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 79  
 QY 61 YNPGLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYA-----MDYWGQGT 115  
 Db 80 YNPGLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYA-----MDYWGQGT 137  
 QY 116 SVTVSS 121  
 Db 138 SVTVSS 143

RESULT 3  
 A49442  
 Ig heavy chain V region (50.1) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
 C:Accession: A49442  
 R:Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapié, L.M.; S  
 Proteins 14, 499-508, 1992  
 A:Title: Crystallization, sequence, and preliminary crystallographic data for an antipep  
 A:Reference number: A49442; MUID:93056166; PMID:1438187  
 A:Accession: A49442  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-107 <STU>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:7-91/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 491; DB 2; Length 107;  
 Best Local Similarity 84.1%; Pred. No. 1.5e-39;  
 Matches 95; Conservative 4; Mismatches 8; Indels 6; Gaps 1;

QY 9 PGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPGLSKR 68  
 Db 1 PGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPGLSKR 60  
 QY 69 LTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVSS 121  
 Db 61 LKISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVSS 107

RESULT 4  
 S26465  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
 C:Accession: S26465  
 R:Kavaler, J.  
 submitted to the EMBL Data Library, April 1991  
 A:Reference number: S26459  
 A:Accession: S26465  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-113 <KAV>  
 A:Cross-references: EMBL:X59115; NID:g51928; PIDN:CAA4184.1; PID:g51929  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:6-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 474.5; DB 2; Length 113;  
 Best Local Similarity 81.4%; Pred. No. 5.9e-36;  
 Matches 92; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 10 GILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPGLSKRL 69  
 Db 1 GILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPGLSKRL 60  
 QY 70 TISKDTSSNOVFLKITSVDTRDTATYTCARRV---SLTAYAMDYWGQGTSTVTV 119

Db 61 TISKDTSSNOVFLKITSVDTRDTATYTCARRAGGYGNYGFDVWGAGTIVTV 113

RESULT 5  
 S26328  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
 C:Accession: S26328  
 R:Stark, S.E.; Caton, A.J.  
 J. Exp. Med. 174, 613-624, 1991  
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e  
 A:Reference number: S26309; MUID:91341421; PMID:1908510  
 A:Accession: S26328  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-116 <STA>  
 A:Cross-references: EMBL:X59198; NID:g52074; PIDN:CAA41908.1; PID:g1334038  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:11-95/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 472.5; DB 2; Length 116;  
 Best Local Similarity 79.3%; Pred. No. 9.3e-38;  
 Matches 92; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 6 ESGPILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPGL 65  
 Db 2 ESGPILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPGL 61  
 QY 66 KSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVSS 121  
 Db 62 KSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVSS 116

RESULT 6  
 S31513  
 Ig heavy chain - human  
 C:Species: Homo sapiens (man)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
 C:Accession: S31513  
 R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
 submitted to the EMBL Data Library, December 1992  
 A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA aut  
 A:Reference number: S31509  
 A:Accession: S31513  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-138 <CHA>  
 A:Cross-references: EMBL:X69861; NID:g33084; PIDN:CAA49495.1; PID:g33085  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:30-114/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 471; DB 2; Length 138;  
 Best Local Similarity 73.0%; Pred. No. 1.6e-37;  
 Matches 89; Conservative 15; Mismatches 16; Indels 2; Gaps 1;

QY 1 QVTLKESGPILOPQSTLSLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
 Db 16 QVTLKESGPILOPQSTLSLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 75  
 QY 61 YNPGLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARR---VSLTAYAMDYWGQGTSTV 118  
 Db 76 YNPGLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARR---VSLTAYAMDYWGQGTSTV 135  
 QY 119 VS 120  
 Db 136 VS 137

RESULT 7

## S09959

IG heavy chain V region (31-9D) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 23-Jul-1999  
C/Accession: S09959  
R/Lawler, A.M.; Lin, P.S.; Gearhart, P.J.  
Eur. J. Immunol. 20, 771-777, 1990  
A>Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies  
A/Reference number: S09955; MUID:90269328; PMID:2347362  
A/Accession: S09959  
A/Molecule type: mRNA  
A/Residues: 1-121 <REI>  
A/Cross-references: EMBL:X51847; NID:G55247; PIDN:CAA36140.1; PID:G930215  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 460; DB 2; Length 121;  
Best Local Similarity 74.4%; Pred. No. 1.5e-36;  
Matches 90; Conservative 10; Mismatches 21; Indels 0; Gaps 0;  
QY 1 QVTLKESGPGILOPSQTLISLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHYWDDDKR 60  
Db 1 QVTLKESGPGILOPSQTLISLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHYWDDDKR 60  
QY 61 YNPFLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAYMDYWGQTSVTVS 120  
Db 61 YNPFLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAYMDYWGQTSVTVS 120  
QY 121 S 121  
Db 121 S 121

## RESULT 8

A49002  
IG heavy chain V region, rheumatoid factor RF antibody - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C/Accession: A49002  
R/Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.  
Arthritis Rheum. 35, 900-904, 1992  
A>Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene  
A/Reference number: A49002; MUID:92352481; PMID:1322670  
A/Accession: A49002  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-124 <STU>  
A/Cross-references: GB:M90808; NID:G185515; PIDN:AAA52989.1; PID:G567176  
A/Experimental source: EBV-transformed lymphoblastoid cell line SH23  
A/Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBIP:110262)  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 454.5; DB 2; Length 124;  
Best Local Similarity 70.2%; Pred. No. 5.1e-36;  
Matches 87; Conservative 16; Mismatches 18; Indels 3; Gaps 2;  
QY 1 QVTLKESGPGILOPSQTLISLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHYWDDDKR 60  
Db 1 QVTLKESGPGILOPSQTLISLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHYWDDDKR 60  
QY 61 YNPFLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAY --AMDYWGQTSV 117  
Db 61 YNPFLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAY --AMDYWGQTSV 120  
QY 118 TVSS 121  
Db 121 TVSS 124

## RESULT 9

## B25913

IG heavy chain precursor V region (BFL23) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 16-Aug-1996  
C/Accession: B25913  
R/Lawler, A.M.; Lin, P.S.; Gearhart, P.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987  
A>Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes  
A/Reference number: A94148; MUID:87175692; PMID:3104915  
A/Accession: B25913  
A/Molecule type: DNA  
A/Residues: 1-103 <LAW>  
A/Note: the authors translated the codon TGT for residue 11 as Ser  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:19-103/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 448; DB 2; Length 103;  
Best Local Similarity 85.9%; Pred. No. 1.7e-35;  
Matches 85; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
QY 1 QVTLKESGPGILOPSQTLISLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHYWDDDKR 60  
Db 5 QVTLKESGPGILOPSQTLISLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHYWDDDKR 64  
QY 61 YNPFLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCAR 99  
Db 65 YNPFLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCAR 103

## RESULT 10

S69339  
IG heavy chain V region precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C/Accession: S69339; S72664  
R/Khamlichi, A.A.; Aucoeur, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A>Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A/Reference number: S69339; MUID:95262687; PMID:7744049  
A/Accession: S69339  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-374 <KHA>  
A/Cross-references: EMBL:X81695  
R/Khamlichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A/Reference number: S72664  
A/Accession: S72664  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-140, 'C', 142-374 <KH2>  
A/Cross-references: EMBL:X81695  
C/Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 68.9%; Score 436; DB 2; Length 374;  
Best Local Similarity 66.4%; Pred. No. 9.8e-34;  
Matches 83; Conservative 17; Mismatches 19; Indels 6; Gaps 2;  
QY 1 QVTLKESGPGILOPSQTLISLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHYWDDDKR 60  
Db 20 QVTLKESGPGILOPSQTLISLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHYWDDDKR 79  
QY 61 YNPFLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAYMDY ---WGQTS 116  
Db 80 YNPFLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAYMDY ---WGQTS 137

Query Match 68.9%; Score 436; DB 2; Length 374;  
Best Local Similarity 66.4%; Pred. No. 9.8e-34;  
Matches 83; Conservative 17; Mismatches 19; Indels 6; Gaps 2;  
QY 1 QVTLKESGPGILOPSQTLISLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHYWDDDKR 60  
Db 20 QVTLKESGPGILOPSQTLISLTCFSGFSLSTSGMGVSWIRQPSGKGLEWLAHYWDDDKR 79  
QY 61 YNPFLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAYMDY ---WGQTS 116  
Db 80 YNPFLSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARVSLTAYMDY ---WGQTS 137  
QY 117 TVSS 121  
Db 138 TVSS 142

## RESULT 11

## GIHUCO

IG heavy chain V-II region (Cor) - human (tentative sequence)  
C:Species: Homo sapiens (man)  
C:Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 31-Mar-2000  
C:Accession: A02089  
R:Press, E.M.; Hogg, N.M.  
Biochem. J. 117, 641-660, 1970  
A:Title: The amino acid sequences of the Fd fragments of two human gamma heavy chains.  
A:Reference number: A90250; MUID:70258837; PMID:5449120  
A:Accession: A02089  
A:Molecule type: protein  
A:Residues: 1-120 <PRE>  
C:Comment: This chain was isolated from an IgG1 myeloma protein.  
C:Genetics:  
A:Gene: GDB:IGHV@  
A:Cross-references: GDB:128528; OMIM:147070  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; pyroglutamic acid  
F:15-96/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:22-94/Disulfide bonds: #status experimental  
F:62/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 66.3%; Score 419.5; DB 1; Length 120;  
Best Local Similarity 68.3%; Pred. No. 9.9e-33;  
Matches 84; Conservative 15; Mismatches 19; Indels 5; Gaps 2;  
QY 1 QVTLKESGPGILQPSQTLSTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHYWDDDKR 60  
DB 1 QVTLRESGPALVKPTQTLTLCTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHYWDDDKY 60  
QY 61 YNPILSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAY--MDYWGQTSVT 118  
DB 61 YNTSLKRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAY--MDYWGQTSVT 117  
QY 119 VSS 121  
DB 118 VSS 120

## RESULT 12

A36005  
IG heavy chain V region (M60) - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1990 #sequence\_revision 13-Sep-1991 #text\_change 16-Dec-1998  
C:Accession: A36005  
R:Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150; 1990  
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A:Reference number: A36005; MUID:90349571; PMID:2117273  
A:Accession: A36005  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-121 <SCH>  
A:Cross-references: GB:M34027  
C:Genetics:  
A:Gene: GDB:IGHV1  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 412; DB 2; Length 121;  
Best Local Similarity 66.9%; Pred. No. 5.1e-32;  
Matches 81; Conservative 15; Mismatches 25; Indels 0; Gaps 0;  
QY 1 QVTLKESGPGILQPSQTLSTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHYWDDDKR 60  
DB 1 EVTLRESGPALVKPTQTLTLCTLYGFSLSSTSGMGVSWIRQPSGKGLWLAHYWDDDKY 60  
QY 61 YNPILSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYMDYWGQTSVTVS 120

Db 61 YSTSLKRLTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYMDYWGQTSVTVS 120  
QY 121 S 121  
Db 121 S 121

## RESULT 13

S18555  
IG heavy chain V region precursor (VII-5) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 06-Jun-1997 #text\_change 21-Jul-2000  
C:Accession: S18555  
R:Shin, E.K.; Matsuda, F.; Nagaoaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; F  
EMBO J. 10, 3641-3645, 1991  
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: c  
A:Reference number: S18551; MUID:92037524; PMID:1935993  
A:Accession: S18555  
A:Molecule type: DNA  
A:Residues: 1-119 <SHI>  
A:Cross-references: EMBL:X62111; NID:g37839; PIDN:CAA44021.1; PID:g3980125  
C:Genetics:  
A:Insertions: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-119/Product: Ig heavy chain V region (VII-5) #status predicted <MAT>  
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 64.8%; Score 410; DB 2; Length 119;  
Best Local Similarity 75.0%; Pred. No. 7.7e-32;  
Matches 75; Conservative 14; Mismatches 11; Indels 0; Gaps 0;  
QY 1 QVTLKESGPGILQPSQTLSTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHYWDDDKR 60  
DB 20 QITLKESGPTLVKPTQTLTLCTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHYWDDDKR 79  
QY 61 YNPILSKRLTISKDTSSNOVFLKITSVDTRDTATYTCARR 100  
DB 80 YSPILSKRLTITKDTSSNOVFLKITSVDTRDTATYTCARR 119

## RESULT 14

MEHLWC  
IG heavy chain V-II region (MCE) - human  
C:Species: Homo sapiens (man)  
C:Date: 14-Nov-1983 #sequence\_revision 22-Nov-1983 #text\_change 02-Sep-1997  
C:Accession: A02092  
R:Gerber-Jenson, B.; Kazin, A.; Kehoe, J.M.; Scheffel, C.; Erickson, B.W.; Litman, G.W.  
J. Immunol. 126, 1212-1216, 1981  
A:Title: Molecular basis for the temperature-dependent insolubility of cryoglobulins. X  
A:Reference number: A02092; MUID:8118242; PMID:6780622  
A:Accession: A02092  
A:Molecule type: protein  
A:Residues: 1-125 <GER>  
A:Note: This chain was derived from a monoclonal IgM cryoimmunoglobulin  
C:Genetics:  
A:Gene: GDB:IGHV@  
A:Cross-references: GDB:128528; OMIM:147070  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid  
F:15-99/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 64.3%; Score 407; DB 1; Length 125;  
Best Local Similarity 63.2%; Pred. No. 1.6e-31;  
Matches 79; Conservative 17; Mismatches 25; Indels 4; Gaps 1;  
QY 1 QVTLKESGPGILQPSQTLSTCSFSGFSLSTSGMGVSWIRQPSGKGLWLAHYWDDDKR 60  
DB 1 QITLKESGPTLVKPTQTLTLCTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHYWDDDKR 60





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 17:48:21 ; Search time 11 Seconds  
(without alignments)  
517.294 Million cell updates/sec

Title: US-09-759-112a-7  
Perfect score: 633  
Sequence: 1 QVTLKSGPGILQPSQTLSL.....SLTAYAMDYWGQTSVTVSS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	419.5	66.3	120	1 HV2B_HUMAN	P01815 homo sapien
2	407	64.3	125	1 HV2D_HUMAN	P01817 homo sapien
3	402.5	63.6	147	1 HV2H_HUMAN	P04438 homo sapien
4	395	62.4	121	1 HV2E_HUMAN	P01818 homo sapien
5	384	60.7	144	1 HV43_MOUSE	P01819 mus musculus
6	371	58.6	119	1 HV2C_HUMAN	P01816 homo sapien
7	358.5	56.6	126	1 HV2A_HUMAN	P01814 homo sapien
8	353	55.8	137	1 HV46_MOUSE	P01822 mus musculus
9	327	51.7	115	1 HV44_MOUSE	P01820 mus musculus
10	317	50.1	129	1 HV2F_HUMAN	P01824 mus musculus
11	315.5	49.8	135	1 HV02_XENLA	P20957 xenopus lae
12	312.5	49.4	116	1 HV60_MOUSE	P18531 mus musculus
13	309.5	48.9	146	1 HV21_HUMAN	P06331 homo sapien
14	306.5	48.4	126	1 HV3K_HUMAN	P01772 homo sapien
15	305	48.2	117	1 HV2G_HUMAN	P01825 mus musculus
16	302	47.7	121	1 HV3J_HUMAN	P18532 mus musculus
17	299.5	47.3	116	1 HV61_MOUSE	P01771 homo sapien
18	299.5	47.3	122	1 HV3G_HUMAN	P01768 homo sapien
19	299.5	47.3	136	1 HV16_MOUSE	P01783 mus musculus
20	298	47.1	113	1 HV47_MOUSE	P01823 mus musculus
21	293	46.3	111	1 HV45_MOUSE	P01821 mus musculus
22	288	45.5	117	1 HV62_MOUSE	P18533 mus musculus
23	287.5	45.4	122	1 HV3H_HUMAN	P01769 homo sapien
24	287	45.3	136	1 HV01_XENLA	P20956 xenopus lae
25	278.5	44.0	119	1 HV40_MOUSE	P01810 mus musculus
26	278	43.9	119	1 HV31_HUMAN	P01770 homo sapien
27	275.5	43.5	119	1 HV37_MOUSE	P01807 mus musculus
28	273	43.1	117	1 HV41_MOUSE	P01811 mus musculus
29	272.5	43.0	119	1 HV38_MOUSE	P01808 mus musculus
30	271.5	42.9	116	1 HV3T_HUMAN	P01781 homo sapien
31	271	42.8	117	1 HV42_MOUSE	P01812 mus musculus
32	266	42.0	119	1 HV3L_HUMAN	P01773 homo sapien
33	262.5	41.5	114	1 HV3E_HUMAN	P01763 homo sapien

34	262.5	41.5	119	1 HV3M_HUMAN	P01774 homo sapien
35	261	41.2	115	1 HV3D_HUMAN	P01765 homo sapien
36	261	41.2	115	1 HV3F_HUMAN	P01767 homo sapien
37	260.5	41.2	118	1 HV3V_HUMAN	P04119 homo sapien
38	259.5	41.0	122	1 HV20_MOUSE	P01789 mus musculus
39	256.5	40.5	119	1 HV3N_HUMAN	P01775 homo sapien
40	256	40.4	118	1 HV39_MOUSE	P01809 mus musculus
41	256	40.4	123	1 HV24_MOUSE	P01793 mus musculus
42	256	40.4	142	1 HV01_RAT	P01805 rattus norv
43	255	40.3	123	1 HV23_MOUSE	P01792 mus musculus
44	255	40.3	123	1 HV25_MOUSE	P01794 mus musculus
45	254.5	40.2	115	1 HV3S_HUMAN	P01780 homo sapien

ALIGNMENTS

RESULT 1  
HV2B\_HUMAN  
ID HV2B\_HUMAN STANDARD; PRT; 120 AA.  
AC P01815;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region COR.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=70258837; PubMed=5449120;  
RA Press E.M., Hogg N.M.;  
RT "The amino acid sequences of the Pd fragments of two human gamma-1  
heavy chains";  
RL Biochem. J. 117:641-660 (1970).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
PROTEIN.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02089; GIHUCO.  
DR HSP; P01825; 7FAB.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 110 IG-LIKE  
FT MOD\_RES 1 94 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFD 22 94  
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .).  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;

Query Match	66.3%;	Score	419.5;	DB 1;	Length	120;			
Best Local Similarity	68.3%;	Pred. No.	2.5e-36;						
Matches	84;	Conservative	15;	Mismatches	19;	Indels	5;	Gaps	2
QY	1	QVTLKESGPGILQPSQTLSLTCSFGSLSTSGMVGSVIRQPSGKGLEWLAIHYWDDDKR	60						
Db	1	QVTLRESGPALVKETQTLTLCTFSGSLSTGTCVGVIRQPPGKGLEWLARIDWDDDKY	60						
QY	61	YNPLKSLRTISKDTSSNQVFLKITSVDRDTATYTCARRVSLTAYA--MDYWGQTSVT	118						
Db	61	YNTSLETRLTISKDTSRNQVVL---TMDPVDVATYTCARITVTPAPAGYMDVWGRGTFVT	117						
QY	119	VSS 121							
Db	118	VSS 120							

```

RESULT 2
HV2D_HUMAN HV2D_HUMAN STANDARD; PRT; 125 AA.
AC P01817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region MCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=81118242; PubMed=6790622;
RA Gerber-Jenson B., Kazin A., Kenoe J.M., Scheffel C., Erickson B.W.,
RA Litman G.W.;
RT "Molecular basis for the temperature-dependent insolubility of
RT cryoglobulins. X. The amino acid sequence of the heavy chain variable
RL J. Immunol. 126:1212-1216(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM
CC CRYOGLOBULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02092; MEHUMC.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19 IG HEAVY CHAIN V-II REGION SESS.
FT DOMAIN 20 147 V SEGMENT.
FT DOMAIN 119 132 D SEGMENT.
FT DOMAIN 133 147 J SEGMENT.
FT NON_TER 147 147
SQ SEQUENCE 125 AA; 13783 MW; 7A1ADF4C40F47BB5 CRC64;

Query Match 64.3%; Score 407; DB 1; Length 125;
Best Local Similarity 63.2%; Pred. No. 5e-35;
Matches 79; Conservative 17; Mismatches 25; Indels 4; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLISLTCFSGFSLSTSGVSGVSWIRQPSGKLEWLAIHYDDDKR 60
Db 1 QITLKESGPTLVKPTETLTCTCFSGFSLSTSGVSGVSWIRQPSGKALEWLAFINWDDNKR 60
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYCAR-----RVSLTAYAMYDYGQTS 116
Db 61 YSPSLRSLRGTGKDTSRNQVLLTINMDPVDSTGYTCAHRPPWRFTGNLGGFDXWGQGLT 120
QY 117 VTVSS 121
Db 121 VTVSS 125

RESULT 3
HV2H_HUMAN HV2H_HUMAN STANDARD; PRT; 147 AA.
AC P04438;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region SESS precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

```

SEQUENCE FROM N.A.
RP MEDLINE=84298107; PubMed=6089186;
RX Takahashi N., Noma T., Honjo T.;
RT "Rearranged immunoglobulin heavy chain variable region (VH)
RT pseudogene that deletes the second complementarity-determining
RT region.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
DR PIR; A02090; G2HUCS.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19 IG HEAVY CHAIN V-II REGION SESS.
FT DOMAIN 20 147 V SEGMENT.
FT DOMAIN 119 132 D SEGMENT.
FT DOMAIN 133 147 J SEGMENT.
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16323 MW; FCBDB3D00FB6666 CRC64;

Query Match 63.6%; Score 402.5; DB 1; Length 147;
Best Local Similarity 62.3%; Pred. No. 1.8e-34;
Matches 76; Conservative 16; Mismatches 23; Indels 7; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLISLTCFSGFSLSTSGVSGVSWIRQPSGKLEWLAIHYDDDKR 60
Db 20 QVNLRSGPALVKATHTLTCTCFSGVSVNTRGMSVSWIRQPSGKALEWLARDWDDKY 79
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYCAR-----RVSLTAYAMYDYGQ 113
Db 80 YGTSLETRLTISKDTSKNQVVLKYNMDPADTATYTCARMQVTWREVMTSNFADWQ 139
QY 114 GT 115
Db 140 GT 141

RESULT 4
HV2E_HUMAN HV2E_HUMAN STANDARD; PRT; 121 AA.
AC P01818;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region HE.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=70114712; PubMed=5264153;
RA Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;
RT "Subgroups of amino acid sequences in the variable regions of
RT immunoglobulin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
CC -1- MISCELLANEOUS: THIS GAMMA-1 CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02093; G1HUHE.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.

```

```
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT MOD_RES 1 120 IG-LIKE.
FT NON_TER 121 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;

Query Match 62.4%; Score 395; DB 1; Length 121;
Best Local Similarity 61.5%; Pred. No. 8.3e-34;
Matches 75; Conservative 20; Mismatches 25; Indels 2; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLISLTCFSFSLSTSGMGVSWIRQPSGKGLEWLAH-IYWDK 59
DB 1 QVTLKENGPTLVKPTETLTCTLSGLSLTDDGAVGWIRQPGRALEWLAHLLYWDK 60

QY 60 RYNSPLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMYWGQTSVTV 119
DB 61 RFSPLKSLRTVTRDTSKNQVLTMTNDFVDATYTCVHRPRT-LAPDVWGQTKVAV 119

QY 120 SS 121
DB 120 SS 121

RESULT 5
HV43_MOUSE STANDARD; PRT; 144 AA.
AC P01819;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774259;
RA Sakano H., Maki R., Kuroiwa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR ENBL; V00768; CAA24149.1; -.
DR PIR; A02094; G2MS14.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION MOPC 141.
FT CHAIN 20 144 IG-LIKE.
FT DOMAIN 20 130
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;
```

```
Query Match 60.7%; Score 384; DB 1; Length 144;
Best Local Similarity 60.9%; Pred. No. 1.4e-32;
Matches 78; Conservative 17; Mismatches 23; Indels 10; Gaps 3;

QY 1 QVTLKESGPGILQPSQTLISLTCFSFSLSTSGMGVSWIRQPSGKGLEWLAHLYWDK 60
DB 20 QVQLKESGPGILVAPQSLSITCTVSGFSL--TCGVNVRVQPPGKGLEWLTGTWNGSTD 77

QY 61 YNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAY-----AMYWGQ 113
DB 78 YNSTLKSLRTITKDNKSKQVFLKMNLSQTDTRATYCA-SVSIYYGRSKDYFTLTDWGQ 136

QY 114 GTSVTSS 121
DB 137 GTSVTSS 144

RESULT 6
HV2C_HUMAN STANDARD; PRT; 119 AA.
AC P01816;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region DAW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "The amino acid sequences of the Fd fragments of two human gamma-1
RT heavy chains.";
RL Biochem. J. 117:641-660(1970).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
CC SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02091; G1HUDW.
DR HSSP; P01789; 1MCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 113 IG-LIKE.
FT MOD_RES 1 113 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match 58.6%; Score 371; DB 1; Length 119;
Best Local Similarity 61.3%; Pred. No. 2.4e-31;
Matches 76; Conservative 15; Mismatches 25; Indels 8; Gaps 3;
```

```
QY 1 QVTLKESGPGILQPSQTLISLTCFSFSLSTSGMGVSWIRQPSGKGLEWLAHLYWD---D 57
DB 1 QVTLRESGPGALVRPTQTLTCTCTFSGFSLSGEIMCVAMIRQPPGEALEWLA---WDILND 57

QY 58 DKRYNPSLKSLRTISKDTSSNOVFLKITSVDTRDTATYTCARRVSLTAYAMYWGQTSV 117
DB 58 DKYYCASLETRAVSKDTSKNQVVLNMTVPGDTATYTCAR--SCGQYFDYWGQILV 115

QY 118 TVSS 121
DB 116 TVSS 119
```

```

RESULT 7
HV2A_HUMAN  STANDARD;          PRT;   126 AA.
AC  P01814;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Ig heavy chain V-II region OV.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=74005511; PubMed=4742735;
RA  Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A.;
RT  'Complete amino acid sequence of the Mu heavy chain of a human IgM
RT  immunoglobulin.';
RL  Science 182:287-291(1973).
CC  -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC  MACROGLOBULIN.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR  PIR; A02088; MHUOU.
DR  HSSP; P01825; 7FAB.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding activity; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS00835; IG LIKE; 1.
KW  Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT  DOMAIN 1 113 IG-LIKE.
FT  MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT  DISULFID 22 97
FT  NON_TER 126 126
FT  SEQUENCE 126 AA; 14276 MW; A85C0BB0DABC296F CRC64;

Query Match      56.6%; Score 358.5; DB 1; Length 126;
Best Local Similarity 60.3%; Pred. No. 4.9e-30;
Matches 76; Conservative 19; Mismatches 26; Indels 5; Gaps 2;

QY  1 QVTLKSGPILQPSQTLISLTSFSGSLSTSGVSWIRQPSGKLEWIAHYWDDKR 60
DB  1 QVTLTSGPALVPKQPLTLTCTFSGSLSTSRMYSWIRRPFGKALEWLAIRIBBDK 60
QY  61 YNPSLKRSLTISKDTSSNOVFLKITSVDTRDTATYTCARRV-SLTA- ---YAMDYWGQT 115
DB  61 WSTSLRSLTSKNDKSNQVLLIMINVPVDTATYTCARVNSVMAGYVYVYVYVWVGKGT 120
QY  116 SVTVSS 121
DB  121 TVTVSS 126

RESULT 8
HV46_MOUSE  STANDARD;          PRT;   137 AA.
AC  P01822;
DT  21-JUL-1986 (Rel. 01, Created)
DT  01-AUG-1992 (Rel. 23, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Ig heavy chain V region MOPC 315 precursor.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89239351; PubMed=2497341;

```

```

RA  Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT  "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT  gene segment.";
RL  Mol. Immunol. 26:431-434 (1989).
RN  [2]
RP  SEQUENCE OF 1-31.
RX  MEDLINE=78094475; PubMed=414225;
RA  Jilka R.L., Pestka S.;
RT  "Amino acid sequence of the precursor region of MOPC-315 mouse
RT  immunoglobulin heavy chain.";
RL  Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN  [3]
RP  SEQUENCE OF 1-21.
RX  MEDLINE=79148758; PubMed=428562;
RA  Schechter I., Wolf O., Zemell R., Burstein Y.;
RT  "Structure and function of immunoglobulin genes and precursors.";
RL  Fed. Proc. 38:1839-1845(1979).
RN  [4]
RP  SEQUENCE OF 19-136.
RX  MEDLINE=74170779; PubMed=4524622;
RA  Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT  "Amino-acid sequence of the variable region of the heavy (alpha)
RT  chain of a mouse myeloma protein with anti-hapten activity.";
RL  Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN  [5]
RP  REVISION TO 53.
RX  MEDLINE=77244979; PubMed=268248;
RA  Hood L., Margolies M.N., Givol D., Zakut R.;
RT  Unpublished results, cited by:
RL  Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL  Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC  -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC  PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL; M27638; AAA61337.1; -.
DR  EMBL; X07880; CAA30727.1; -.
DR  PIR; P0102; AVMS35.
DR  HSSP; P01825; 7FAB.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS00835; IG LIKE; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL 1 18
FT  CHAIN 19 137
FT  DOMAIN 19 48
FT  DOMAIN 49 54
FT  DOMAIN 55 68
FT  DOMAIN 69 84
FT  DOMAIN 85 116
FT  DOMAIN 117 126
FT  DOMAIN 127 137
FT  DISULFID 40 114
FT  CONFLICT 15 15
FT  CONFLICT 15 15
FT  CONFLICT 77 78
FT  CONFLICT 102 102
FT  CONFLICT 123 123
FT  NON_TER 137 137
FT  SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match      55.8%; Score 353; DB 1; Length 137;
Best Local Similarity 59.2%; Pred. No. 2e-29;

```

Matches 71; Conservative 19; Mismatches 28; Indels 2; Gaps 2;  
 QY 2 VTLKESGPGILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDDKEY 61  
 Db 20 VQLQESGPGILVPSQSLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDDKEY 78  
 QY 62 NPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTSS 121  
 Db 79 NPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTSVTSS 137  
 RESULT 9  
 HV44\_MOUSE  
 ID HV44\_MOUSE STANDARD; PRT; 115 AA.  
 AC P01820;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region P14 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81012133; PubMed=6774258;  
 RA Sakano H., Maki R., Kurosewa Y., Roeder W., Tonegawa S.;  
 RT "Two types of somatic recombination are necessary for the generation  
 of complete immunoglobulin heavy-chain genes.";  
 RL Nature 286:676-683(1980).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC ENBL; V00767; CAA24148.1; -  
 DR PIR; A02095; HVMS14.  
 DR PDB; 1A7N; 29-APR-98.  
 DR PDB; 1A7O; 29-APR-98.  
 DR PDB; 1A7P; 29-APR-98.  
 DR PDB; 1A7R; 29-APR-98.  
 DR PDB; 1G7H; 17-JAN-01.  
 DR PDB; 1G7I; 17-JAN-01.  
 DR PDB; 1G7J; 17-JAN-01.  
 DR PDB; 1G7M; 17-JAN-01.  
 DR PDB; 43C9; 24-JUL-02.  
 DR PDB; 43CA; 24-JUL-02.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig-MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Signal; 3D-structure.  
 FT SIGNAL 1  
 FT CHAIN 13  
 FT DOMAIN 20 115 IG HEAVY CHAIN V REGION P14.  
 FT NON TER 115 >115 IG-LIKE.  
 SQ SEQUENCE 115 AA; 12447 MW; 7569DDA4A4843D500 CRC64;

Query Match 51.7%; Score 327; DB 1; Length 115;  
 Best Local Similarity 54.3%; Pred. No. 7.6e-27;  
 Matches 63; Conservative 14; Mismatches 19; Indels 2; Gaps 1;  
 QY 1 QVTLKESGPGILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDDKEY 60  
 Db 20 QVQLKESGPGILVAPSSQSLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDDKEY 77

QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYYCA 98  
 Db 78 YNSALKSRLSISKNSKNSQVFLKNSLCTDDTATYYCA 115  
 RESULT 10  
 HV2F\_HUMAN  
 ID HV2F\_HUMAN STANDARD; PRT; 129 AA.  
 AC P01824;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region WAH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=8222235; PubMed=6806818;  
 RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;  
 RT "Complete amino acid sequence of the delta heavy chain of human  
 immunoglobulin D.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA  
 PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02099; D2HWA.  
 DR HSSP; P01825; 7FAB.  
 DR GlycoSuiteDB; P01824; -  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006985; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig-MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 113 IG-LIKE.  
 FT NON TER 129 129  
 SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;  
 Query Match 50.18; Score 317; DB 1; Length 129;  
 Best Local Similarity 49.6%; Pred. No. 9.2e-26;  
 Matches 64; Conservative 18; Mismatches 39; Indels 8; Gaps 1;  
 QY 1 QVTLKESGPGILOPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDDKEY 60  
 Db 1 RLQLQESGPGILVPSQSLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDDKEY 60  
 QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAY-----ANDYWG 112  
 Db 61 YNPSLRGRVTSVDTSRNQFSLNLSRMSAADTATYYCARGNPPPPYDYGTSDDGIDVWG 120  
 QY 113 QGTSVTVSS 121  
 Db 121 QGTTVTVSS 129  
 RESULT 11  
 HV02\_XENLA  
 ID HV02\_XENLA STANDARD; PRT; 135 AA.  
 AC P20957;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region XIc14 precursor (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus.

```

NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
MEDLINE=88176921; PubMed=2451244;
Schwager J., Mikoryak C.A., Steiner L.A.;
"Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
from cDNA sequence: implications for evolution of immunoglobulin
domains."
Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249 (1988).
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
EMBL; J03632; AAA49791.1; -
PIR; B31933; B31933.
HSP; P01810; 2FBU.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN 1 1
FT DOMAIN 1 1
FT CHAIN 1 1
IG HEAVY CHAIN V REGION XIG14.
IG-LIKE.
FT SIGNAL 1 1
FT CHAIN 1 1
FT CHAIN 1 1
FT DOMAIN 1 1
FT NON_TER 1 1
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 49.8%; Score 315.5; DB 1; Length 135;
Best Local Similarity 52.1%; Pred. No. 1.4e-25;
Matches 62; Conservative 20; Mismatches 34; Indels 3; Gaps 2;

QY 3 TLKESGPGILQPSQTLSTCSFSGSLTSGMGVSWIQPSGKGLWLAHIYWDCKRYN 62
DB 20 TLQESGPGILQPSQTLSTCSFSGSLTSGMGVSWIQPSGKGLWLAHIYWDCKRYN 77
QY 63 PSLSKRLTISKDTSSNOVFLKITSVDTRTATYCYARRVSLTAYAWDYGQTSVTGSS 121
DB 78 DSLKNRVTIKNGKKQVLIQNGMEVKDTAMTYCAREYA-SGYNFDWGGQGTMTVTS 135

RESULT 12
HV60 MOUSE STANDARD; PRT; 116 AA.
AC P18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAN=BALB/CJ;
MEDLINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response."
J. Exp. Med. 169:2007-2019 (1989).
PIR; J0509; HVMS31.
HSP; P01825; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
```

```

InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116
FT DOMAIN 19 48
FT DOMAIN 49 53
FT DOMAIN 54 67
FT DOMAIN 68 84
FT DOMAIN 85 116
FT DISULFID 40 114
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 49.4%; Score 312.5; DB 1; Length 116;
Best Local Similarity 60.2%; Pred. No. 2.4e-25;
Matches 59; Conservative 18; Mismatches 20; Indels 1; Gaps 1;

QY 2 VTILKESGPGILQPSQTLSTCSFSGSLTSGMGVSWIQPSGKGLWLAHIYWDCKRY 61
DB 20 VQLQESGPGILQPSQTLSTCSFSGSLTSGMGVSWIQPSGKGLWLAHIYWDCKRY 78
QY 62 NPSLSKRLTISKDTSSNOVFLKITSVDTRTATYCYARR 99
DB 79 NPSLSKRLTISKDTSSNOVFLKITSVDTRTATYCYARR 116

RESULT 13
HV21 HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=85205332; PubMed=3922855;
Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
"A cloned human immunoglobulin heavy chain gene with a novel direct-
repeat sequence in 5' flanking region."
Gene 33:181-189 (1985).
PIR; A02101; GIH02.
HSP; P01825; 7FAB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; P:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146
FT DOMAIN 20 117
FT DOMAIN 118 127
FT DOMAIN 128 146
FT DISULFID 42 115
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 48.9%; Score 309.5; DB 1; Length 146;
Best Local Similarity 52.3%; Pred. No. 6.3e-25;
Matches 67; Conservative 14; Mismatches 38; Indels 9; Gaps 2;
```

```
QY 1 QVTLKESGPIQLPSQTLSTLCSFGSFLSTSGMGVSWIQPSGKGLWLAHIYWDK 60
Db 21 QVQLQWAGLVKPSSETLSLTCAVFGSP--SGYVSWIQPPGRLGLEWICINHG 78
QY 61 YNPSLKRLTIKDTSSNOVFLKITSVDTDTATYTCAREVSLTA-----Y 113
Db 79 YKTSLKSRVITSLDTSKLFLSLSSVTAADTAVYTCARGLLGGWVDVYYG 138
QY 114 GTSVTYSS 121
Db 139 GTTIVTSS 146

RESULT 14
HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-II region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=684994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "three-dimensional structure determination of antibodies. Primary
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RN Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
[2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RL immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RL and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02055; GIHUKL.
DR PDB; 2FB4; 12-JUL-89.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT TURN 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 64
FT HELIX 65 66
FT TURN 68 67
FT STRAND 73 77
FT TURN 74 77
```

```
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 48.4%; Score 306.5; DB 1; Length 126;
Best Local Similarity 50.4%; Pred. No. 1.1e-24;
Matches 65; Conservative 18; Mismatches 35; Indels 11; Gaps 4;

QY 1 QVTLKESGPIQLPSQTLSTLCSFGSFLSTSGMGVSWIQPSGKGLWLAHIYWD 58
Db 1 QVQLVESGGGVQVQGRSLRLSCSSGSGIFSSYAM--YVVRQAPGKGLWVA-I 57
QY 59 KRYNPSLKRLTIKDTSSNOVFLKITSVDTDTATYTCARR-----VSL 112
Db 58 QYADSVKGRFTISRDNKNTFLQMDSLRPDTGVYFCARDGGHGFCSASCFGP 117
QY 113 QGTSVTYSS 121
Db 118 QGTPVTYSS 126

RESULT 15
HV2G_HUMAN STANDARD; PRT; 117 AA.
AC P01825;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-II region NEWM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77242302; PubMed=407927;
RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
RT "Amino acid sequence of the VH region of a human myeloma
RL immunoglobulin (IgG New).";
RL Biochemistry 16:3412-3420(1977).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RX MEDLINE=78066916; PubMed=618887;
RA Saul F.A., Amzel L.M., Poljak R.J.;
RT "Preliminary refinement and structural analysis of the Fab fragment
RL from human immunoglobulin new at 2.0-A resolution.";
RL J. Biol. Chem. 253:585-597(1978).
CC 1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90404; GIHUNM.
DR PDB; 2FAB; 31-JAN-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 111
FT MOD_RES 1 1
FT STRAND 3 7
FT TURN 11 12
```





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 18:55:07 ; Search time 36.6667 Seconds  
(without alignments)  
851.574 Million cell updates/sec

Title: US-09-759-112a-7

Perfect score: 633

Sequence: 1 QVTLKESGPILQPSQTLSTL.....SLTAYAMDYWGQTSVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virvius.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	74.4	121	4 Q9UL96	Q9UL96 homo sapien
2	398.5	63.0	121	11 Q9NKG4	Q9NKG4 mus musculus
3	370.5	58.5	482	11 Q9IX92	Q9IX92 mus musculus
4	361.5	57.1	496	4 Q96XX8	Q96XX8 homo sapien
5	361	57.0	119	4 Q9UL73	Q9UL73 homo sapien
6	356	56.2	97	4 Q43234	Q43234 homo sapien
7	354.5	56.0	613	4 Q96EY0	Q96EY0 homo sapien
8	343	54.2	479	11 Q9NM22	Q9NM22 mus musculus
9	341	53.9	588	4 Q8WDX4	Q8WDX4 homo sapien
10	341	53.9	597	4 Q9BU10	Q9BU10 homo sapien
11	341	53.9	618	4 Q96AA6	Q96AA6 homo sapien
12	338	53.4	597	4 Q9BQ88	Q9BQ88 homo sapien
13	337.5	53.3	150	4 Q95973	Q95973 homo sapien
14	331.5	52.4	122	4 Q9UL75	Q9UL75 homo sapien
15	307.5	48.6	130	4 Q81ZD7	Q81ZD7 homo sapien
16	305.5	48.3	147	4 Q9Y509	Q9Y509 homo sapien

17	302.5	47.8	613	4 Q8WUK1	Q8WUK1 homo sapien
18	301.5	47.6	473	4 Q8TC63	Q8TC63 homo sapien
19	295	46.6	113	4 Q9UL90	Q9UL90 homo sapien
20	290	45.8	499	4 Q8NSK4	Q8NSK4 homo sapien
21	288.5	45.6	112	4 Q9HCC1	Q9HCC1 homo sapien
22	284.5	44.9	573	4 Q8WU38	Q8WU38 homo sapien
23	284	44.9	116	4 Q9UL93	Q9UL93 homo sapien
24	280	44.2	493	4 Q8NCL6	Q8NCL6 homo sapien
25	278.5	44.0	122	4 Q9UL84	Q9UL84 homo sapien
26	276.5	43.7	473	11 Q91205	Q91205 mus musculus
27	273.5	43.2	118	4 Q9UL31	Q9UL31 homo sapien
28	272.5	43.0	118	4 Q9UL72	Q9UL72 homo sapien
29	272	43.0	121	4 Q9UL71	Q9UL71 homo sapien
30	272	43.0	131	4 Q9UL88	Q9UL88 homo sapien
31	269.5	42.6	145	11 Q924Q9	Q924Q9 mus musculus
32	269.5	42.6	471	4 Q8TC77	Q8TC77 homo sapien
33	269.5	42.6	484	11 Q8VEA0	Q8VEA0 mus musculus
34	268.5	42.4	298	11 Q9QIF0	Q9QIF0 mus musculus
35	266.5	42.1	145	11 Q924P7	Q924P7 mus musculus
36	265.5	41.9	487	11 Q99KA4	Q99KA4 mus musculus
37	264	41.7	597	4 Q96BB9	Q96BB9 homo sapien
38	263	41.5	468	11 Q99L31	Q99L31 mus musculus
39	262.5	41.5	494	4 Q86K68	Q86K68 homo sapien
40	261.5	41.3	145	11 Q924R1	Q924R1 mus musculus
41	261.5	41.3	469	11 Q8R3V9	Q8R3V9 mus musculus
42	260.5	41.2	145	11 Q924Q6	Q924Q6 mus musculus
43	259.5	41.0	241	11 Q921A6	Q921A6 mus musculus
44	257	40.6	484	11 Q99LA6	Q99LA6 mus musculus
45	256	40.4	118	4 Q9UL74	Q9UL74 homo sapien

## ALIGNMENTS

### RESULT 1

Q9UL96 PRELIMINARY; PRT; 121 AA.  
AC Q9UL96;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035018; AAD56254.1; -;  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 121 AA; 13695 MW; D582D450596DD35 CRC64;

Query Match 74.4%; Score 471; DB 4; Length 121;  
Best Local Similarity 73.6%; Pred. No. 4.3e-44;  
Matches 89; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

Qy 1 QVTLKESGPILQPSQTLSTLTCFSFSLTSGMGVSWIQPSGKGLWLAHYWDDKKR 60

```
Db 1 QVTLKESGPGILOPQSLTCTSPGFSLSLTSGMDVGWIRQPPGKALEWLAHIYWDGDKR 60
QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVTS 120
Db 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 2
Q99NG4 PRELIMINARY; PRT; 121 AA.
AC Q99NG4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
CG Plasmid pHEN1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawlicsek H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
Bautsch W., Koja A., Klos A., Koehl J.,
"Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL J. Immunol. 160:2947-2958(1998).
DR EMBL; AJ222590; CAA10890.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Plasmid.
FT NON TER 1 121
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;

Query Match 63.0%; Score 398.5; DB 11; Length 121;
Best Local Similarity 64.8%; Pred. No. 4.1e-36;
Matches 79; Conservative 17; Mismatches 23; Indels 3; Gaps 2;

QY 1 QVTLKESGPGILOPQSLTCTSPGFSLSLTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
Db 1 QVQLKESGPGILVAPSQSLTCTVSGFPLTSH--GVSWVRQPPGKGLWLGVIWGDNVTK 58
QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTV 119
Db 59 YHSAISRLTSKDNKSKQVFLKNSLQTDATYTCARRHYKYANYAMDYWGQGTSTV 118
QY 120 SS 121
Db 119 SS 120

RESULT 3
Q91X92 PRELIMINARY; PRT; 482 AA.
AC Q91X92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Unknown (Protein for MGC:18822).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011181; AAH11181.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
SQ SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;

Query Match 58.5%; Score 370.5; DB 11; Length 482;
Best Local Similarity 61.2%; Pred. No. 3e-32;
Matches 74; Conservative 17; Mismatches 27; Indels 3; Gaps 2;

QY 1 QVTLKESGPGILOPQSLTCTSPGFSLSLTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
Db 20 QVQLKESGPGILVAPSQSLTCTVSGFALTS--VAISWVRQPPGKGLWLGVIWGTGVTN 77
QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTV 120
Db 78 YNSALKSLTSKDNKSKQVFLKNSLQTDATYTCARRVSLTAYAMDYWGQGTSTV 136
QY 121 S 121
Db 137 S 137

RESULT 4
Q96KX8 PRELIMINARY; PRT; 496 AA.
AC Q96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 57.1%; Score 361.5; DB 4; Length 496;
Best Local Similarity 59.2%; Pred. No. 3.1e-31;
Matches 74; Conservative 17; Mismatches 29; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILOPQSLTCTSPGFSLSLTSGMGVSWIRQPSGKLEWLAHIYWDGDKR 60
Db 20 QVQLKESGPGILVAPSQSLTCTVSGSISSSSYWVRQPPGKLEWLAHIYWDGDKR 79
QY 61 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTV 116
Db 80 YNPGLKSLRTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQGTSTV 138
```

QY 117 VTSS 121  
DB 139 VTSS 143

## RESULT 5

Q9UL73 PRELIMINARY; PRT; 119 AA.  
AC Q9UL73; 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035041; AAD56277.1; -.  
DR HSSP; P01825; TPAB.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 119  
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EA0BE CRC64;

Query Match 57.0%; Score 361; DB 4; Length 119;  
Best Local Similarity 58.7%; Pred. No. 5.5e-32;  
Matches 71; Conservative 16; Mismatches 32; Indels 2; Gaps 1;  
QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
DB 1 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYW--SWIRQPSGKLEWIGIYVSGSTN 58  
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYADYWGQGSVTVS 120  
DB 59 YFSLKSRVTISVDREKQPSLKLSTLAADTAVYFCARLSNKGPFYFDYWGQGLVTVS 118  
QY 121 S 121  
DB 119 S 119

## RESULT 6

O43234 PRELIMINARY; PRT; 97 AA.  
AC O43234;  
DT 01-JUN-1998 (T-EMBLrel. 06, Created)  
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Rheumatoid factor RF-ET13 (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Borretzen M., Natvig J.B., Thompson K.M.;  
RT "Heterogenous Rf structures between and within healthy individuals are not related to HLA DRE1\*0401."  
RL Mol. Immunol. 0:0-0(1997).

DR EMBL; AF035802; AAB8534.1; -.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 97  
SQ SEQUENCE 97 AA; 10748 MW; DDC0BF47B9AA812D CRC64;  
Query Match 56.2%; Score 356; DB 4; Length 97;  
Best Local Similarity 68.0%; Pred. No. 1.5e-31;  
Matches 66; Conservative 16; Mismatches 15; Indels 0; Gaps 0;  
QY 3 TLKESGPGILQPSQTLSTLTCFSGFSLTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYN 62  
DB 1 TLKESGPGALVKPTETLTCTVSGFSLSNRMGVSWIRQPSGKAVEWLAHIFANDEKSYS 60  
QY 63 PSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCAR 99  
DB 61 TSLKSRLTISKDTSKSQVLTMTNMDPMDTATYYCAR 97

## RESULT 7

Q96EY0 PRELIMINARY; PRT; 613 AA.  
AC Q96EY0;  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011857; AAH11857.1; -.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 56.0%; Score 354.5; DB 4; Length 613;  
Best Local Similarity 59.0%; Pred. No. 2.4e-30;  
Matches 72; Conservative 16; Mismatches 31; Indels 3; Gaps 2;  
QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
DB 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYW--SWIRQPSGKLEWIGIYVSGSTN 77  
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRV--SLTAYADYWGQGSVTIV 119  
DB 78 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRV--SLTAYADYWGQGSVTIV 117  
QY 120 SS 121  
DB 138 SS 139  
RESULT 8  
Q99M22 PRELIMINARY; PRT; 479 AA.  
ID Q99M22

```

AC Q9W22;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002091; AAH02091.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51992 MW; 768839A138918892 CRC64;

Query Match 54.2%; Score 343; DB 11; Length 479;
Best Local Similarity 57.0%; Pred. No. 3.2e-29;
Matches 69; Conservative 20; Mismatches 26; Indels 6; Gaps 3;

QY 2 VTLKESGPILQPSOTLSLTCSFSGFSLSTGSGVSWIRQPSGKLEWLAIHYWDDDKR 61
DB 20 VQLQESGVLKPSQSLTSCVTGYSI-TSYIYWNWIRQPKNLEWGVINDGSGNNY 78

QY 62 NPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-YMDYWGQGVTS 120
DB 79 NPSLKNRISITRDTSKNQVFLKINSVTTEDTATYTCASR---GYSWFPNQGQGLTVTS 134

QY 121 S 121
DB 135 A 135

RESULT 9
Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match 53.9%; Score 341; DB 4; Length 588;
Best Local Similarity 55.9%; Pred. No. 6.9e-29;
Matches 71; Conservative 15; Mismatches 33; Indels 8; Gaps 2;

```

```

QY 1 QVTLKESGPILQPSOTLSLTCSFSGFSLSTGSGVSWIRQPSGKLEWLAIHYWDDDKR 60
DB 20 QVQLQWAGLGLKPSSETLSLTGCVGGSF--SGYIYWNWIRQPKNLEWGVINDGSGNNY 77

QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-----YMDYWGQ 114
DB 78 YNPSLKSRLTISVDTSKQSLKLSVNAADTAVYTCARVITRASPGTGRYGMVWGQ 137

QY 115 TSVTVSS 121
DB 138 TTVTVSS 144

RESULT 10
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 53.9%; Score 341; DB 4; Length 597;
Best Local Similarity 55.9%; Pred. No. 7e-29;
Matches 71; Conservative 15; Mismatches 33; Indels 8; Gaps 2;

QY 1 QVTLKESGPILQPSOTLSLTCSFSGFSLSTGSGVSWIRQPSGKLEWLAIHYWDDDKR 60
DB 20 QVQLQWAGLGLKPSSETLSLTGCVGGSF--SGYIYWNWIRQPKNLEWGVINDGSGNNY 77

QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTA-----YMDYWGQ 114
DB 78 YNPSLKSRLTISVDTSKQSLKLSVNAADTAVYTCARVITRASPGTGRYGMVWGQ 137

QY 115 TSVTVSS 121
DB 138 TTVTVSS 144

RESULT 11
Q96AA6 PRELIMINARY; PRT; 618 AA.
AC Q96AA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```



Search completed: January 14, 2004, 19:13:12  
Job time : 40.6667 secs

```
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035039; AAD56275.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match 52.4%; Score 331.5; DB 4; Length 122;
Best Local Similarity 54.4%; Pred. No. 18-28; 32; Indels 7; Gaps 3;
Matches 68; Conservative 18; Mismatches 32; Indels 7; Gaps 3;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSSTGGMVSWIRQSPGKLEWLAHIY----WD 56
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLQSGPGLVKPKGQTLSTLTCASGDSVSSNSAANNWIRQSPGKLEWIGRTYVRSKWY 60

QY 57 DDKRYNPISLKSRLTISKOTSSNOVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQTS 116
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 ND--YRVSVKSRITINPDTSRKNQFSQLNSVTPEDTAVYYCARDLELLG-QPDYWGQGT 117

QY 117 VTVSS 121
Db |||:|||||

QY 118 VTVSS 122
Db |||:|||||

RESULT 15
Q81ZD7 PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;
RT "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
RT Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145445; AN64329.1; -.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 48.6%; Score 307.5; DB 4; Length 130;
Best Local Similarity 50.0%; Pred. No. 4.8e-26;
Matches 85; Conservative 20; Mismatches 36; Indels 9; Gaps 3;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSSTGGMVSWIRQSPGKLEWLAHIY----W 55
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QVQLQSGPGLVKPKGQTLSTLTCVSGSISSSSYWGWIRQSPGKLEWIGSLYSGSTY 60

QY 56 DDKRYNPISLKSRLTISKOTSSNOVFLKITSVDTRDTATYYCARRVSLT---AYA-MDYW 111
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SGSPYVAPSRVRSVILISVDTSKNQLSLRUSVTAADTAVYYCASPTHCSGGGCIAPFQHW 120

QY 112 GQTSVTVSS 121
Db |||:|||||

QY 121 GQGLVTVSS 130
Db |||:|||||
```

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 19:10:12 ; Search time 15.1905 Seconds  
(without alignments)  
337.028 Million cell updates/sec

Title: US-09-759-112A-7

Perfect score: 633

Sequence: 1 QVTLKSGEGLQPSQTLSL.....SLTAYAMDYWGQGTSTVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/2/iaa/53\_COMB.pep.\*
- 3: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*
- 4: /cgn2\_6/prodata/2/iaa/53\_COMB.pep.\*
- 5: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*
- 6: /cgn2\_6/prodata/2/iaa/53\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	569	89.9	140	2	US-08-483-636-4
2	569	89.9	140	2	US-08-483-632-4
3	569	89.9	141	2	US-08-483-636-10
4	569	89.9	141	2	US-08-483-632-10
5	567.5	89.7	246	1	US-08-197-834-7
6	551.5	87.1	122	1	US-08-436-463-14
7	522.5	82.5	139	5	PCT-US95-07372-10
8	521.5	82.4	120	2	US-08-553-501A-88
9	521.5	82.4	120	3	US-09-205-231-88
10	521.5	82.4	139	2	US-08-553-501A-29
11	521.5	82.4	139	3	US-09-205-231-29
12	506.5	80.0	120	2	US-08-290-592B-32
13	505.5	79.9	143	1	US-08-436-463-2
14	504	79.6	108	1	US-08-436-463-17
15	502	79.3	141	2	US-08-483-636-12
16	502	79.3	141	2	US-08-483-632-12
17	500	79.0	121	2	US-08-483-636-64
18	500	79.0	121	2	US-08-483-632-64
19	499.5	78.9	120	5	PCT-US95-10053-29
20	499.5	78.9	120	5	PCT-US96-09448-32
21	499	78.8	108	1	US-08-436-463-15
22	489.5	77.3	120	5	PCT-US95-10053-28
23	489.5	77.3	120	5	PCT-US96-09448-31
24	482	76.1	114	1	US-08-436-463-16
25	470.5	74.3	126	4	US-09-225-322B-4
26	470.5	74.3	126	4	US-09-764-304-4
27	470.5	74.3	141	4	US-09-225-322B-2

28	470.5	74.3	141	4	US-09-764-304-2	Sequence 2, Appli
29	467.5	73.9	120	2	US-08-230-592B-31	Sequence 31, Appl
30	459.5	72.5	120	4	US-09-025-769B-23	Sequence 23, Appl
31	454	71.7	121	4	US-09-025-769B-37	Sequence 37, Appl
32	454	71.7	121	4	US-09-025-769B-61	Sequence 61, Appl
33	445	70.3	123	5	PCT-US95-10053-27	Sequence 27, Appl
34	445	70.3	123	5	PCT-US96-09448-30	Sequence 30, Appl
35	443	70.0	499	3	US-09-049-672A-1	Sequence 1, Appli
36	440.5	69.6	139	2	US-08-553-501A-59	Sequence 59, Appl
37	440.5	69.6	139	3	US-09-205-231-59	Sequence 59, Appl
38	437.5	69.1	139	2	US-08-553-501A-61	Sequence 61, Appl
39	437.5	69.1	139	3	US-09-205-231-61	Sequence 61, Appl
40	436	68.9	123	2	US-08-290-592B-30	Sequence 30, Appl
41	433.5	68.5	120	2	US-08-553-501A-90	Sequence 90, Appl
42	433.5	68.5	120	3	US-09-205-231-90	Sequence 90, Appl
43	431.5	68.2	141	2	US-08-345-321-10	Sequence 10, Appl
44	430.5	68.0	120	2	US-08-553-501A-91	Sequence 91, Appl
45	430.5	68.0	120	3	US-09-205-231-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1  
US-08-483-636-4  
; Sequence 4, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 140 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Protein



US-08-483-636-4

Query Match 89.9%; Score 569; DB 2; Length 140;  
 Best Local Similarity 90.1%; Pred. No. 5.8e-50;  
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 QVTLKESGPGILQPSQTLSTLCSPGSLSTSGMGVSWIROPSGKGLWLAHIYDDDKR 60  
 DB 20 QVTLKESGPGILQPSQTLSTLCSPGSLSTSGMGVSWIROPSGKGLWLAHIYDDDKR 79  
 QY 61 YNPISLKSRLTISKDTSSNQVFLKITSVDTRTATYYCARRVSLTAYAMDYWGQGTSTVTS 120  
 DB 80 YNPISLKSRLTISKDTSSNQVFLKITSVDTRTATYYCARRVSLTAYAMDYWGQGTSTVTS 139  
 QY 121 S 121  
 DB 140 S 140

RESULT 2

US-08-483-632-4  
 ; Sequence 4, Application US/08483632  
 ; Patent No. 5928904  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Holmes, Stephen D.  
 ; APPLICANT: Gross, Mitchell S.  
 ; APPLICANT: Sylvester, Daniel R.  
 ; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
 ; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
 ; NUMBER OF SEQUENCES: 75  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corp./Corporate  
 ; ADDRESSEE: Intellectual Property  
 ; STREET: P.O. Box 1539 / UW2220  
 ; CITY: King of Prussia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19406-0939  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/483,632  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/117366  
 ; FILING DATE: 07-SEP-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/136783  
 ; FILING DATE: 14-OCT-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US/94/10308  
 ; FILING DATE: 07-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sutton, Jeffrey A.  
 ; REGISTRATION NUMBER: 34,028  
 ; REFERENCE/DOCKET NUMBER: P50186-3  
 ; TELEPHONE: (215) 270-5024  
 ; TELEFAX: (215) 270-5090  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 140 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-483-632-4

Query Match 89.9%; Score 569; DB 2; Length 140;  
 Best Local Similarity 90.1%; Pred. No. 5.8e-50;

Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 QVTLKESGPGILQPSQTLSTLCSPGSLSTSGMGVSWIROPSGKGLWLAHIYDDDKR 60  
 DB 20 QVTLKESGPGILQPSQTLSTLCSPGSLSTSGMGVSWIROPSGKGLWLAHIYDDDKR 79  
 QY 61 YNPISLKSRLTISKDTSSNQVFLKITSVDTRTATYYCARRVSLTAYAMDYWGQGTSTVTS 120  
 DB 80 YNPISLKSRLTISKDTSSNQVFLKITSVDTRTATYYCARRVSLTAYAMDYWGQGTSTVTS 139  
 QY 121 S 121  
 DB 140 S 140

RESULT 3

US-08-483-636-10  
 ; Sequence 10, Application US/08483636  
 ; Patent No. 5914110  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Holmes, Stephen D.  
 ; APPLICANT: Gross, Mitchell S.  
 ; APPLICANT: Sylvester, Daniel R.  
 ; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
 ; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
 ; NUMBER OF SEQUENCES: 75  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corp./Corporate  
 ; ADDRESSEE: Intellectual Property  
 ; STREET: P.O. Box 1539 / UW2220  
 ; CITY: King of Prussia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19406-0939  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/483,636  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/117366  
 ; FILING DATE: 07-SEP-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/136783  
 ; FILING DATE: 14-OCT-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US/94/10308  
 ; FILING DATE: 07-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sutton, Jeffrey A.  
 ; REGISTRATION NUMBER: 34,028  
 ; REFERENCE/DOCKET NUMBER: P50186-3  
 ; TELEPHONE: (215) 270-5024  
 ; TELEFAX: (215) 270-5090  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 141 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-483-636-10

Query Match 89.9%; Score 569; DB 2; Length 141;  
 Best Local Similarity 90.1%; Pred. No. 5.9e-50;  
 Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILQPSQTLSTLCSPGSLSTSGMGVSWIROPSGKGLWLAHIYDDDKR 60

Db 21 QVTLKESGPGILOPQSOTLSITCSFGFSLSSTSGMGVSWIRQPSGKGLEWLAHIYWDDEKR 80  
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAAYMDYWGQTSVTVS 120  
Db 81 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVTFYFYFDVWGAGITVTVS 140  
QY 121 S 121  
Db 141 S 141

## RESULT 4

US-08-483-632-10  
; Sequence 10, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,632  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA: PCT/US/94/10308  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 141 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-632-10

Query Match 89.9%; Score 569; DB 2; Length 141;  
Best Local Similarity 90.1%; Pred. No. 5.9e-50;  
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVTLKESGPGILOPQSOTLSITCSFGFSLSSTSGMGVSWIRQPSGKGLEWLAHIYWDDEKR 60  
Db 21 QVTLKESGPGILOPQSOTLSITCSFGFSLSSTSGMGVSWIRQPSGKGLEWLAHIYWDDEKR 80  
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAAYMDYWGQTSVTVS 120

Db 81 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVTFYFYFDVWGAGITVTVS 140  
QY 121 S 121  
Db 141 S 141

## RESULT 5

US-08-197-834-7  
; Sequence 7, Application US/08197834  
; Patent No. 5639455  
; GENERAL INFORMATION:  
; APPLICANT: SHIMAMURA, TOSHIRO  
; APPLICANT: NAKAZAWA, HARUMI  
; APPLICANT: HAMURO, JUNJI  
; TITLE OF INVENTION: IMMUNOSUPPRESSANT  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,834  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 028173/1993  
; FILING DATE: 17-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5639455man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 10-661-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 246 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-197-834-7

Query Match 89.7%; Score 567.5; DB 1; Length 246;  
Best Local Similarity 89.6%; Pred. No. 1.1e-49;  
Matches 112; Conservative 3; Mismatches 5; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILOPQSOTLSITCSFGFSLSSTSGMGVSWIRQPSGKGLEWLAHIYWDDEKR 60  
Db 123 QVTLKESGPGILOPQSOTLSITCSFGFSLSSTSGMGVSWIRQPSGKGLEWLAHIYWDDEKR 182  
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAAYMDYWGQTS 116  
Db 183 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARR-SLYGNWGDYAMDYWGQTS 241  
QY 117 VTSS 121  
Db 242 VTSS 246

## RESULT 6

US-08-436-463-14  
; Sequence 14, Application US/08436463

Patent No. 5760185  
GENERAL INFORMATION:  
APPLICANT: KIMACHI, Kazuhiko  
APPLICANT: MAEDA, Hiroaki  
APPLICANT: NISHIYAMA, Kiyoto  
APPLICANT: TOKIYOSHI, Sachio  
TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/436,463  
FILING DATE: 26-JUN-1995  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 341255/1992  
FILING DATE: 28-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: KIMACHI=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-463-14

Query Match 87.1%; Score 551.5; DB 1; Length 122;  
Best Local Similarity 91.4%; Pred. No. 2.8e-48;  
Matches 106; Conservative 2; Mismatches 7; Indels 1; Gaps 1;  
QY 1 QVTLKESGPGILQPSQTLISLTCSFGSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
Db 8 QVTLKESGPGILQPSQTLISLTCSFGSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 67  
QY 61 YNPISLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGT 116  
Db 68 YNPISLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGT 122

RESULT 7  
PCT-US95-07372-10  
Sequence 10, Application PC/TUS9507372  
GENERAL INFORMATION:  
APPLICANT: Oklahoma Medical Research Foundation  
TITLE OF INVENTION: Calcium Binding Recombinant  
TITLE OF INVENTION: Antibody Against Protein C  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07372  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF106CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 20..139  
OTHER INFORMATION: /note= "Gln at position 20 starts mature peptide."  
PCT-US95-07372-10

Query Match 82.5%; Score 522.5; DB 5; Length 139;  
Best Local Similarity 84.3%; Pred. No. 2.7e-45;  
Matches 102; Conservative 3; Mismatches 15; Indels 1; Gaps 1;  
QY 1 QVTLKESGPGILQPSQTLISLTCSFGSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
Db 20 QVTLKESGPGILQPSQTLISLTCSFGSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 79  
QY 61 YNPISLKSRLTISKDTSSNQVFLKITSVDTRDTATYYCARRVSLTAYAMDYWGQGT 120  
Db 80 YNPVLKSLIISKDTSRKQVFLKIASVDITADTATYYCVRMD-DYDAMDYWGQGT 138  
QY 121 S 121  
Db 139 S 139

RESULT 8  
US-08-553-501A-88  
Sequence 88, Application US/08553501A  
Patent No. 5856135  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: HIRATA, Yuichi  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,501A  
FILING DATE: 20-FEB-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-553-501A-88

Query Match 82.4%; Score 521.5; DB 2; Length 120;  
Best Local Similarity 83.7%; Pred. No. 2.8e-45;  
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;  
QY 1 QVTLKESGPGILOPSQTLSITCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIYWDKDKR 60  
DB 1 QVTLKESGPGILOPSQTLSITCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIWWDKDY 60  
QY 61 YNPALKRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAY--AMDYWGQGTSTV 118  
DB 61 YNPALKGRITISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAY---MEDYDEANDYWGQGTSTV 117  
QY 119 VSS 121  
DB 118 VSS 120

RESULT 9  
US-09-205-231-88  
Sequence 88, Application US/09205231  
Patent No. 6121423  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/205,231  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/553,501  
FILING DATE: 20-FEB-1996  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-205-231-88

Query Match 82.4%; Score 521.5; DB 3; Length 120;  
Best Local Similarity 83.7%; Pred. No. 2.8e-45;  
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;  
QY 1 QVTLKESGPGILOPSQTLSITCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIYWDKDKR 60  
DB 1 QVTLKESGPGILOPSQTLSITCSFSGFSLSTSGMGVSWIRQPSGKLEWLAHIWWDKDY 60  
QY 61 YNPALKRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAY--AMDYWGQGTSTV 118  
DB 61 YNPALKGRITISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAY---MEDYDEANDYWGQGTSTV 117  
QY 119 VSS 121  
DB 118 VSS 120

RESULT 10  
US-08-553-501A-29  
Sequence 29, Application US/08553501A  
Patent No. 5858135  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,501A  
FILING DATE: 20-FEB-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993

ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-553-501A-29

Query Match 82.4%; Score 521.5; DB 2; Length 139;  
Best Local Similarity 83.7%; Pred. No. 3.4e-45;  
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLTLTCSFSGFSLTSGMGVSWIROPSGKLEWLAIHYWDDDKR 60  
DB 20 QVTLKESGPGILQPSQTLTLTCSFSGFSLTSGMGVSWIROPSGKLEWLAIHYWDDDKY 79

QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTTRDTATYYCARRVSLTAY--AMDYWGQGTSTV 118  
DB 80 YNPALKGRLTISKDTSSNQVFLKIASVVTADTATYYCAR---MEDYDEAMDYWGQGTSTV 136

QY 119 VSS 121  
DB 137 VSS 139

RESULT 11  
US-09-205-231-29  
Sequence 29, Application US/09205231  
Patent No. 6121423  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SAITO, Koh  
APPLICANT: HIRATA, Yuichi  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
INTERLEUKIN-6  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/205,231  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,501  
FILING DATE: 20-FEB-1996  
APPLICATION NUMBER: WO PCT/JP94/00859  
FILING DATE: 30-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-129787  
FILING DATE: 31-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/177/AAOK  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-205-231-29

Query Match 82.4%; Score 521.5; DB 3; Length 139;  
Best Local Similarity 83.7%; Pred. No. 3.4e-45;  
Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

QY 1 QVTLKESGPGILQPSQTLTLTCSFSGFSLTSGMGVSWIROPSGKLEWLAIHYWDDDKR 60  
DB 20 QVTLKESGPGILQPSQTLTLTCSFSGFSLTSGMGVSWIROPSGKLEWLAIHYWDDDKY 79

QY 61 YNPSLKSLRTISKDTSSNQVFLKITSVDTTRDTATYYCARRVSLTAY--AMDYWGQGTSTV 118  
DB 80 YNPALKGRLTISKDTSSNQVFLKIASVVTADTATYYCAR---MEDYDEAMDYWGQGTSTV 136

QY 119 VSS 121  
DB 137 VSS 139

RESULT 12  
US-08-290-592E-32  
Sequence 32, Application US/08290592E  
Patent No. 5824307  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, L.  
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against  
Respiratory Syncytial Virus  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &  
ADDRESSEE: OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,592E  
FILING DATE: August 15, 1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/813,372  
FILING DATE: December 23, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 469201-257  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-290-592E-32

Query Match 80.0%; Score 506.5; DB 2; Length 120;

Best Local Similarity 81.8%; Pred. No. 9.1e-44;  
Matches 99; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
DB 1 QVELQESGPGILQPSQTLSTLTCFSFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKD 60  
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120  
DB 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 119  
QY 121 S 121  
DB 120 S 120

## RESULT 13

US-08-436-463-2  
; Sequence 2, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: KIMACHI=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 143 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-436-463-2

Query Match 79.9%; Score 505.5; DB 1; Length 143;  
Best Local Similarity 79.8%; Pred. No. 1.4e-43;  
Matches 99; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
DB 20 QVTLKESGPGILQPSQTLSTLTCFSFSLSTSGMGAGWIRQPSGKLEWLAIHYWDDVKR 79  
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSV 117  
DB 80 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSV 139

QY 118 TVSS 121  
DB 140 TVSA 143

## RESULT 14

US-08-436-463-17  
; Sequence 17, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: KIMACHI=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-436-463-17

Query Match 79.6%; Score 504; DB 1; Length 108;  
Best Local Similarity 90.8%; Pred. No. 1.4e-43;  
Matches 99; Conservative 1; Mismatches 7; Indels 2; Gaps 2;

QY 9 PGILQPSQTLSTLTCFSFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKRYNPSLKSR 68  
DB 1 PGILQPSQTLSTLTCFSFSLSTSGMG-SWIRQPSGKLEWLAIHYWDDDKRYNPSLKSR 59  
QY 69 LTISKDTSSNQVFLKITSVDTRDTATYTCARRV-SLTAYAMDYWGQTS 116  
DB 60 LTISKDTSSNQVFLKITSVDTRDTATYTCARRV-SLTAYAMDYWGQTS 108

## RESULT 15

US-08-483-636-12  
; Sequence 12, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.

APPLICANT: Sylvester, Daniel R.  
 TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
 TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
 NUMBER OF SEQUENCES: 75  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SmithKline Beecham Corp./Corporate  
 ADDRESSEE: Intellectual Property  
 STREET: P.O. Box 1539 / UW2220  
 CITY: King of Prussia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19406-0939  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/483,636  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/117366  
 FILING DATE: 07-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/136783  
 FILING DATE: 14-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US/94/10308  
 FILING DATE: 07-SEP-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sutton, Jeffrey A.  
 REGISTRATION NUMBER: 34,028  
 REFERENCE/DOCKET NUMBER: P50186-3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 270-5024  
 TELEFAX: (215) 270-5030  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 141 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-483-636-12

Query Match 79.3%; Score 502; DB 2; Length 141;  
 Best Local Similarity 76.9%; Pred. No. 3.1e-43;  
 Matches 93; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY	1	QVTLKESGPGILQPSOTLSITCSFGSLSTGCMGVSWIRQPSGKLEWLAIHYWDDDKR	60
Db	21	QVTLRESGALVAPTQTTLTCTCTFSGSLSTGCMGVSWIRQPSGKLEWLAIHYWDDDKR	80
QY	61	YNPSLKSRLTISKDTSNQVFLKITSVDTRDTATYYCAERVSILTAYMDYWGQGTSTVTS	120
Db	81	YNPSLKSRLTISKDTSNQVFLKITSVDTRDTATYYCAERVSILTAYMDYWGQGTSTVTS	140
QY	121	S	121
Db	141	S	141

Search completed: January 14, 2004, 19:14:23  
 Job time : 16.1905 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 19:13:23 ; Search time 169.19 Seconds  
(without alignments)  
146.239 Million cell updates/sec

Title: US-09-759-112a-7  
Perfect score: 633  
Sequence: 1 QVTLKESGFIQPSQTLSTL.....SLTAYAMDYWGQTSVTYS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 762491 seqs, 20448190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	633	100.0	121	11	US-09-759-112a-7
2	569	89.9	140	10	US-09-879-461-4
3	569	89.9	141	10	US-09-879-461-10
4	555	87.7	123	11	US-09-995-529-12
5	551	87.0	142	12	US-10-010-942B-16
6	525	82.9	119	12	US-10-323-903-3
7	506.5	80.0	120	10	US-09-158-120A-32
8	506.5	80.0	143	9	US-09-881-823-8
9	502	79.3	141	10	US-09-879-461-12
10	498.5	78.9	120	15	US-10-011-531-3
11	470.5	74.3	126	9	US-09-764-304-4
12	470.5	74.3	126	12	US-10-166-626-4
13	470.5	74.3	126	15	US-10-265-713-4
14	470.5	74.3	141	9	US-09-764-304-2
15	470.5	74.3	141	12	US-10-166-626-2

16	470.5	74.3	141	15	US-10-265-713-2	Sequence 2, Appli
17	468.5	74.0	120	9	US-09-796-848A-4	Sequence 4, Appli
18	468.5	74.0	120	10	US-09-771-415-2	Sequence 2, Appli
19	468.5	74.0	450	10	US-09-996-288-208	Sequence 208, App
20	468.5	74.0	450	11	US-09-996-285-208	Sequence 208, App
21	467.5	73.9	120	10	US-09-158-120A-31	Sequence 31, Appl
22	466.5	73.7	120	10	US-09-771-415-18	Sequence 18, Appl
23	466.5	73.7	120	10	US-09-771-415-24	Sequence 20, Appl
24	466.5	73.7	120	10	US-09-771-415-24	Sequence 20, Appl
25	466.5	73.7	120	10	US-09-771-415-26	Sequence 24, Appl
26	466.5	73.7	450	10	US-09-996-288-210	Sequence 26, Appl
27	466.5	73.7	450	10	US-09-996-288-240	Sequence 210, App
28	466.5	73.7	450	11	US-09-996-265-210	Sequence 240, App
29	466.5	73.7	450	11	US-09-996-265-240	Sequence 240, App
30	465.5	73.5	450	10	US-09-996-288-238	Sequence 238, App
31	465.5	73.5	450	10	US-09-996-288-242	Sequence 242, App
32	465.5	73.5	450	10	US-09-996-288-244	Sequence 244, App
33	465.5	73.5	450	10	US-09-996-288-246	Sequence 246, App
34	465.5	73.5	450	11	US-09-996-285-238	Sequence 246, App
35	465.5	73.5	450	11	US-09-996-265-242	Sequence 238, App
36	465.5	73.5	450	11	US-09-996-265-244	Sequence 244, App
37	465.5	73.5	450	11	US-09-996-265-246	Sequence 246, App
38	464.5	73.4	120	10	US-09-771-415-22	Sequence 22, Appl
39	463.5	73.2	450	10	US-09-996-288-248	Sequence 248, App
40	463.5	73.2	450	11	US-09-996-285-248	Sequence 248, App
41	463	73.1	119	12	US-10-156-255-7	Sequence 7, Appli
42	462.5	73.1	120	9	US-09-796-848A-2	Sequence 2, Appli
43	462.5	73.1	120	10	US-09-996-288-7	Sequence 7, Appli
44	462.5	73.1	120	11	US-09-996-265-7	Sequence 7, Appli
45	462.5	73.1	120	12	US-10-020-354-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-759-112a-7  
; Sequence 7, Application US/09759112a  
; Publication No. US20030100741A1  
; GENERAL INFORMATION:  
; APPLICANT: Mueller, Sybille  
; APPLICANT: Kohler, Heinz  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING VARIABLE REGIONS OF HEAVY AND LIGHT  
; TITLE OF INVENTION: OF MONOCLONAL ANTIBODY 1P7, AN ANTI-IDIOTYPIC ANTIBODY REACTIVE  
; TITLE OF INVENTION: ANTIBODIES  
; FILE REFERENCE: 200-013  
; CURRENT APPLICATION NUMBER: US/09/759,112A  
; CURRENT FILING DATE: 2001-01-11  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; TYPE: PRT  
; ORGANISM: mouse  
; US-09-759-112a-7

Query Match	100.0%	Score	633	DB	11	Length	121
Best Local Similarity	100.0%	Pred. No.	1.3e-54				
Matches	121	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	QVTLKESGFIQPSQTLSTLCTCSFGSLSSTSGMGSWIRQPSGKGLWLAHIYDDDKR	60				
Db	1	QVTLKESGFIQPSQTLSTLCTCSFGSLSSTSGMGSWIRQPSGKGLWLAHIYDDDKR	60				
QY	61	YNPSLKSRLTISKDSSNOVFLKITSVDRTRATYYCARRVSLTAYAMDYWGQTSVTYS	120				
Db	61	YNPSLKSRLTISKDSSNOVFLKITSVDRTRATYYCARRVSLTAYAMDYWGQTSVTYS	120				
QY	121	S	121				
Db	121	S	121				



## RESULT 2

US-09-879-461-4  
; Sequence 4, Application US/09879461  
; Publication No. US20020193575A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; Gross, Mitchell S.  
; Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: Corporate Intellectual Property, UW2220 - 709  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,461  
; FILING DATE: 12-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/612,929  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/136,783  
; FILING DATE: 14-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 140 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-879-461-4

Query Match 89.9%; Score 569; DB 10; Length 140;  
Best Local Similarity 90.1%; Pred. No. 2.8e-48;  
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 1 QVTLKESGFGILQPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAIYWDGDKR 60  
Db 20 QVTLKESGFGILQPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAIYWDGDKR 79  
QY 61 YNPFLSKRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120  
Db 80 YNPFLSKRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 139  
QY 121 S 121  
Db 140 S 140

## RESULT 3

US-09-879-461-10  
; Sequence 10, Application US/09879461  
; Publication No. US20020193575A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; Gross, Mitchell S.  
; Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: Corporate Intellectual Property, UW2220 - 709  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,461  
; FILING DATE: 12-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/612,929  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/136,783  
; FILING DATE: 14-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 141 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-879-461-10

Query Match 89.9%; Score 569; DB 10; Length 141;  
Best Local Similarity 90.1%; Pred. No. 2.8e-48;  
Matches 109; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 1 QVTLKESGFGILQPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAIYWDGDKR 60  
Db 21 QVTLKESGFGILQPSQTLTLTCSFGSFLSTSGMGVSWIRQPSGKLEWLAIYWDGDKR 80  
QY 61 YNPFLSKRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120  
Db 81 YNPFLSKRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 140  
QY 121 S 121  
Db 141 S 141

## RESULT 4

US-09-995-529-12  
; Sequence 12, Application US/09995529  
; Publication No. US20030099655A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Tang, Ying  
; TITLE OF INVENTION: Humanized Collagen Antibodies and  
; Related Methods  
; FILE REFERENCE: P-IX 4976  
; CURRENT APPLICATION NUMBER: US/09/995,529  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-995-529-12

Query Match 87.7%; Score 555; DB 11; Length 123;  
Best Local Similarity 87.8%; Pred. No. 5.7e-47;  
Matches 108; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
Db 1 QVTLKESGPGILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
QY 61 YNPGLKSLRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSL--TAYANDYWGQGTSTV 118  
Db 61 YNPGLKSLRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSL--TAYANDYWGQGTSTV 120  
QY 119 VSS 121  
Db 121 VSS 123

## RESULT 5

US-10-010-942B-16  
Sequence 16, Application US/10010942B  
Publication No. US20030165496A1  
GENERAL INFORMATION:  
APPLICANT: Basi, Gurik  
APPLICANT: Saldanha, Jose  
APPLICANT: Vednock, Ted  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
TITLE OF INVENTION: BETA AMYLOID PEPTIDE  
FILE REFERENCE: ELN-002  
CURRENT APPLICATION NUMBER: US/10/010,942B  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: US 60/251,892  
PRIOR FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 142  
TYPE: PRT  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)...(19)  
US-10-010-942B-16

Query Match 87.0%; Score 551; DB 12; Length 142;  
Best Local Similarity 87.8%; Pred. No. 1.7e-46;  
Matches 108; Conservative 1; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
Db 20 QATLKESGPGILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 79  
QY 61 YNPGLKSLRLTISKDTSSNQVFLKITSVDTRDTATYTCARR--VSLTAYANDYWGQGTSTV 118  
Db 80 YNPGLKSLRLTISKDTSSNQVFLKITSVDTRDTATYTCARR--VSLTAYANDYWGQGTSTV 139  
QY 119 VSS 121  
Db 140 VSS 142

## RESULT 6

US-10-323-903-3  
Sequence 3, Application US/10323903  
Publication No. US2003022832A1  
GENERAL INFORMATION:  
APPLICANT: FISCHER, GERALD WALTER

APPLICANT: SCHUMAN, RICHARD F.  
APPLICANT: MOND, JAMES JACOB  
APPLICANT: KOKAI-KUN, JOHN FITZGERALD  
APPLICANT: FOSTER, SIMON  
APPLICANT: STINSON, JEFFREY R.  
TITLE OF INVENTION: MULTIFUNCTIONAL MONOCLONAL ANTIBODIES DIRECTED TO  
FILE REFERENCE: 07787,0059  
CURRENT APPLICATION NUMBER: US/10/323,903  
CURRENT FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: 60/343,444  
PRIOR FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 09/097,055  
PRIOR FILING DATE: 1998-06-15  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic M130  
OTHER INFORMATION: heavy chain antibody  
US-10-323-903-3

Query Match 82.9%; Score 525; DB 12; Length 119;  
Best Local Similarity 83.1%; Pred. No. 4.8e-44;  
Matches 103; Conservative 5; Mismatches 8; Indels 8; Gaps 2;  
QY 1 QVTLKESGPGILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
Db 1 QVTLKESGPGILQPSQTLTLTCSFSGFSLSTSGMGVSWIRQPSGKLEWLAIHYWDDDKR 60  
QY 61 YNPGLKSLRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAND--YWGQGTSTV 117  
Db 61 YNPGLKSLRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAND--YWGQGTSTV 115  
QY 118 TVSS 121  
Db 116 TVSA 119

## RESULT 7

US-09-158-120A-32  
Sequence 32, Application US/09158120A  
Patent No. US20020102257A1  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, L.  
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
ADDRESSEE: STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: P160  
OPERATING SYSTEM: Windows95  
SOFTWARE: MS Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/158,120A  
FILING DATE: September 21, 1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/290,592  
FILING DATE: August 15, 1994  
APPLICATION NUMBER: 07/813,372  
FILING DATE: December 23, 1991

```
ATTORNEY/AGENT INFORMATION:
NAME: OIsteiN, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 469201-367
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-158-120A-32

Query Match      80.0%; Score 506.5; DB 10; Length 120;
Best Local Similarity 81.8%; Pred.No.3.2e-42;
Matches 99; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVTLKESGFGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHWDDDKR 60
DB 1 QVELQESGFGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHWDDDKD 60
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120
DB 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 119
QY 121 S 121
DB 120 S 120

RESULT 8
US-09-881-823-8
Sequence 8, Application US/09881823
Patent No. US20020068066A1
GENERAL INFORMATION:
APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
APPLICANT: WIMS, LETITIA
APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 8
LENGTH: 143
TYPE: PRT
ORGANISM: Murine
US-09-881-823-8

Query Match      80.0%; Score 506.5; DB 9; Length 143;
Best Local Similarity 81.1%; Pred.No.3.9e-42;
Matches 99; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVTLKESGFGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHWDDDKR 60
DB 20 QVTLKESGFGILQPSQTLSTLTCFSGFSLRTYIGVGVIRQPSGKLEWLAIHWDDNKY 79
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAY-AMDYWGQTSVTV 119
DB 80 YNTVLKSRLTISKDTSSNQVFLKIASVDTRDTATYTCARRVSLTAY-AMDYWGQTSVTV 139
QY 120 SS 121
DB 140 SS 141
```

```
RESULT 9
US-09-879-461-12
Sequence 12, Application US/09879461
Publication No. US20020193575A1
GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,461
FILING DATE: 12-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,929
FILING DATE: <unknown>
APPLICATION NUMBER: US 08/136,783
FILING DATE: 14-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-879-461-12

Query Match      79.3%; Score 502; DB 10; Length 141;
Best Local Similarity 76.9%; Pred.No.1.1e-41;
Matches 93; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVTLKESGFGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKLEWLAIHWDDDKR 60
DB 21 QVTLRESGPAVKEPTQTTLTCTFSGFSLSTSGMGVSWIRQPSGKLEWLAIHWDDDKR 80
QY 61 YNPSLKSRLTISKDTSSNQVFLKITSVDTRDTATYTCARRVSLTAYAMDYWGQTSVTVS 120
DB 81 YNPSLKSRLTISKDTSSNQVFLTMTNPDVDTATYTCARRVTFYWFVDFWVGKTEPTVS 140
QY 121 S 121
DB 141 S 141

RESULT 10
US-10-011-931-3
Sequence 3, Application US/10011931
Publication No. US20030026806A1
GENERAL INFORMATION:
APPLICANT: WITTE, ALISON
```

```

; APPLICANT: VARNUM, BRIAN C.
; APPLICANT: QIAN, ZUEMING
; APPLICANT: VEZINA, CHRIS
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BINDING TO IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
; FILE REFERENCE: A-731
; CURRENT APPLICATION NUMBER: US/10/011,931
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 60/244,118
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-011-931-3

Query Match      78.9%; Score 499.5; DB 15; Length 120;
Best Local Similarity 81.0%; Pred. No. 1.5e-41;
Matches 98; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVTLKESGPILOPQSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 1 QVTLKESGPILOPQSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDES 60
QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYYCARRVSLTAYAMDYMGQGTSTVTS 120
DB 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYYCARRVSLTAYAMDYMGQGTSTVTS 120
QY 121 S 121
DB 120 S 120

RESULT 11
US-09-764-304-4
; Sequence 4, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-09-764-304-4

Query Match      74.3%; Score 470.5; DB 9; Length 126;
Best Local Similarity 75.4%; Pred. No. 1.1e-38;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPILOPQSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 5 QVTLKESGPILOPQSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLANVWNSDAKY 64
QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYYCARRVSLTA-YAMDYMGQGTSTVTV 119
DB 65 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYYCARRVSLTA-YAMDYMGQGTSTVTV 124
QY 120 SS 121
DB 125 SS 126

RESULT 12
US-10-166-626-4
; Sequence 4, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-10-166-626-4

Query Match      74.3%; Score 470.5; DB 12; Length 126;
Best Local Similarity 75.4%; Pred. No. 1.1e-38;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPILOPQSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 5 QVTLKESGPILOPQSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLANVWNSDAKY 64
QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYYCARRVSLTA-YAMDYMGQGTSTVTV 119
DB 65 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYYCARRVSLTA-YAMDYMGQGTSTVTV 124
QY 120 SS 121
DB 125 SS 126

RESULT 13
US-10-265-713-4
; Sequence 4, Application US/10265713
; Publication No. US2003095964A1
; GENERAL INFORMATION:
```

```

Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPILOPQSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 5 QVTLKESGPILOPQSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLANVWNSDAKY 64
QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYYCARRVSLTA-YAMDYMGQGTSTVTV 119
DB 65 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYYCARRVSLTA-YAMDYMGQGTSTVTV 124
QY 120 SS 121
DB 125 SS 126

RESULT 12
US-10-166-626-4
; Sequence 4, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma
US-10-166-626-4

Query Match      74.3%; Score 470.5; DB 12; Length 126;
Best Local Similarity 75.4%; Pred. No. 1.1e-38;
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPILOPQSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLAHIYWDGDKR 60
DB 5 QVTLKESGPILOPQSTLSLTCSFSGFSLSTSGMGVSWIRQPSGKGLEWLANVWNSDAKY 64
QY 61 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYYCARRVSLTA-YAMDYMGQGTSTVTV 119
DB 65 YNPSLKSLRLTISKDTSSNQVFLKITSVTRDTATYYCARRVSLTA-YAMDYMGQGTSTVTV 124
QY 120 SS 121
DB 125 SS 126

RESULT 13
US-10-265-713-4
; Sequence 4, Application US/10265713
; Publication No. US2003095964A1
; GENERAL INFORMATION:
```

APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: HASEGAWA, MAMORU  
APPLICANT: MIYAJI, HIROMASA  
APPLICANT: KUMANA, YOSHIHISA  
FILE REFERENCE: 249-101  
CURRENT APPLICATION NUMBER: US/10/265,713  
PRIOR FILING DATE: 2002-10-08  
PRIOR APPLICATION NUMBER: US/09/225,322  
PRIOR FILING DATE: 1999-01-05  
PRIOR APPLICATION NUMBER: US 08/454,680  
PRIOR FILING DATE: 1995-03-31  
PRIOR APPLICATION NUMBER: US 08/408,133  
PRIOR FILING DATE: 1995-03-21  
PRIOR APPLICATION NUMBER: US 08/292,178  
PRIOR FILING DATE: 1994-08-17  
PRIOR APPLICATION NUMBER: US07/947,674  
PRIOR FILING DATE: 1992-09-17  
PRIOR APPLICATION NUMBER: JP 3-238375  
PRIOR FILING DATE: 1991-09-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 126  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma  
US-10-265-713-4

Query Match 74.3%; Score 470.5; DB 15; Length 126;  
Best Local Similarity 75.4%; Pred. No. 1.1e-38;  
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDKR 60  
DB 5 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTYGMVGIWIRQSSGKGLWLANVWSDAKY 64  
QY 61 YNPSLKRLTISKDTSSNQVFLKITSVDTRDTATYICARRVSLTA-YANDYWGQGTSTVTV 119  
DB 65 YNPSLKRLTISKDTSSNQVFLKITSVDTRDTATYICARRVSLTA-YANDYWGQGTSTVTV 124  
QY 120 SS 121  
DB 125 SS 126

RESULT 14  
US-09-764-304-2  
Sequence 2, Application US/09764304  
Patent No. US20020025036A1  
GENERAL INFORMATION:  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: HASEGAWA, MAMORU  
APPLICANT: MIYAJI, HIROMASA  
APPLICANT: KUMANA, YOSHIHISA  
FILE REFERENCE: 249-101  
CURRENT APPLICATION NUMBER: US/09/764,304  
PRIOR FILING DATE: 2001-01-19  
EARLIER APPLICATION NUMBER: 09/225,322  
EARLIER FILING DATE: 1999-01-05  
EARLIER APPLICATION NUMBER: US 08/454,680  
EARLIER FILING DATE: 1995-03-31  
EARLIER APPLICATION NUMBER: US 08/408,133  
EARLIER FILING DATE: 1995-03-21  
EARLIER APPLICATION NUMBER: US 08/292,178  
EARLIER FILING DATE: 1994-08-17  
EARLIER APPLICATION NUMBER: US07/947,674  
EARLIER FILING DATE: 1992-09-17  
EARLIER APPLICATION NUMBER: JP 3-238375

EARLIER FILING DATE: 1991-09-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 141  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Rat hybridoma  
US-09-764-304-2

Query Match 74.3%; Score 470.5; DB 9; Length 141;  
Best Local Similarity 75.4%; Pred. No. 1.3e-38;  
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDKR 60  
DB 20 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTYGMVGIWIRQSSGKGLWLANVWSDAKY 79  
QY 61 YNPSLKRLTISKDTSSNQVFLKITSVDTRDTATYICARRVSLTA-YANDYWGQGTSTVTV 119  
DB 80 YNPSLKRLTISKDTSSNQVFLKITSVDTRDTATYICARRVSLTA-YANDYWGQGTSTVTV 139  
QY 120 SS 121  
DB 140 SS 141

RESULT 15  
US-10-166-626-2  
Sequence 2, Application US/10166626  
Publication No. US20030166876A1  
GENERAL INFORMATION:  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: HASEGAWA, MAMORU  
APPLICANT: MIYAJI, HIROMASA  
APPLICANT: KUMANA, YOSHIHISA  
FILE REFERENCE: 249-101  
CURRENT APPLICATION NUMBER: US/10/166,626  
CURRENT FILING DATE: 2002-06-12  
PRIOR APPLICATION NUMBER: US/09/225,322B  
PRIOR FILING DATE: 1999-01-05  
PRIOR APPLICATION NUMBER: US 08/454,680  
PRIOR FILING DATE: 1995-03-31  
PRIOR APPLICATION NUMBER: US 08/408,133  
PRIOR FILING DATE: 1995-03-21  
PRIOR APPLICATION NUMBER: US 08/292,178  
PRIOR FILING DATE: 1994-08-17  
PRIOR APPLICATION NUMBER: US07/947,674  
PRIOR FILING DATE: 1992-09-17  
PRIOR APPLICATION NUMBER: JP 3-238375  
PRIOR FILING DATE: 1991-09-18  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 141  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Rat hybridoma  
US-10-166-626-2

Query Match 74.3%; Score 470.5; DB 12; Length 141;  
Best Local Similarity 75.4%; Pred. No. 1.3e-38;  
Matches 92; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTSGMGVSWIRQPSGKGLWLAHIYWDGDKR 60  
DB 20 QVTLKESGPGILQPSQTLSTLTCFSGFSLSTYGMVGIWIRQSSGKGLWLANVWSDAKY 79  
QY 61 YNPSLKRLTISKDTSSNQVFLKITSVDTRDTATYICARRVSLTA-YANDYWGQGTSTVTV 119

Search completed: January 14, 2004, 19:25:04  
Job time : 170.19 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 15:52:50 ; Search time 1621.9 Seconds  
(without alignments)  
8323.656 Million cell updates/sec

Title: US-09-759-112a-22

Perfect score: 330

Sequence: 1 gacattgtgctcaccaattc.....ggaccaagctgagctgaaa 330

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_cm.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_vt.\*
- 31: em\_hgt.\*
- 32: em\_hgt\_inv.\*
- 33: em\_hgt\_inv.\*
- 34: em\_hgt\_mus.\*
- 35: em\_hgt\_pln.\*
- 36: em\_hgt\_rod.\*
- 37: em\_hgt\_mam.\*
- 38: em\_hgt\_vrt.\*
- 39: em\_sy.\*
- 40: em\_hgtgo\_hum.\*
- 41: em\_hgtgo\_mus.\*
- em\_hgtgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	293	88.8	333	6	E30643
2	293	88.8	363	10	MUSL202IGK
3	293	88.8	714	6	BD090542
4	293	88.8	714	6	BD090651
5	293	88.8	714	6	E40005
6	293	88.8	714	6	E40813
7	293	88.8	714	6	E43359
8	293	88.8	877	6	E31225
9	293	88.8	925	6	E30616
10	293	88.8	925	6	E30617
11	289.8	87.8	354	10	MUSL711IGKV
12	289.8	87.8	363	10	MUSL931IGKV
13	289.8	87.8	393	10	AF045518
14	288.2	87.3	333	6	E07408
15	288.2	87.3	333	10	MMAC005355
16	288.2	87.3	363	10	MUSL341IGKV
17	286.6	86.8	333	6	AR014069
18	286.6	86.8	333	10	S54207
19	286.6	86.8	831	6	AX392999
20	286.2	86.7	350	10	MUSIGKABBC
21	285	86.4	333	10	MUSIGL5B
22	285	86.4	333	10	S42888
23	285	86.4	334	6	E02169
24	285	86.4	336	10	MMIGLC310
25	285	86.4	336	10	MMIGLC404
26	285	86.4	393	10	S50265
27	285	86.4	396	10	AF207705
28	285	86.4	744	12	AF402256
29	283.6	85.9	333	10	AY173024
30	283.4	85.9	333	10	AF112403
31	283.4	85.9	333	10	AF321952
32	283.4	85.9	336	10	MUSIGKAAW
33	283.4	85.9	393	6	AR144017
34	281.8	85.4	336	10	MMU012372
35	280.8	85.1	360	10	MUSIGKAF
36	280.8	85.1	900	6	I08223
37	277.6	84.1	351	10	MUSIGKABBH
38	276	83.6	333	10	MMVL1E10
39	276	83.6	353	10	MUSIGKABBD
40	275.4	83.5	336	10	MMIGLC413
41	275.4	83.5	768	6	BD090559
42	275.4	83.5	768	6	BD090668
43	275.4	83.5	768	6	E40022
44	275.4	83.5	768	6	E40830
45	275.4	83.5	768	6	E43376

ALIGNMENTS

RESULT 1  
E30643

LOCUS E30643 333 bp DNA linear PAT 18-JUN-2001  
DEFINITION Antibody and nucleic acid encoding the same.

ACCESSION E30643

VERSION E30643.1 GI:13017209

KEYWORDS JP 1999332563-A/30.

SOURCE Mus sp.

ORGANISM Mus sp.

REFERENCE  
1 (bases 1 to 333)  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Mitsuharu, O., Takayuki, K. and Ixuo, M.

TITLE Antibody and nucleic acid encoding the same

JOURNAL Patent: JP 1999332563-A 30 07-DEC-1999;





CC Drug containing humanized anti-Fas antibody  
 FH Key Location/Qualifiers  
 FT CDS (1) . (714)  
 FT mat\_peptide (61) . (714)  
 FT sig\_peptide (1) . (60)

## FEATURES

source  
 1..714  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 BASE COUNT 200 a 184 c 173 g 157 t  
 ORIGIN

Query Match 88.8%; Score 293; DB 6; Length 714;  
 Best Local Similarity 94.6%; Pred. No. 1.2e-88;  
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;  
 QY 1 GACATTGTGCTCACCACCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGCGAGAGGCCACC 60  
 Db 61 GACATTGTGCTGACCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGCGAGAGGCCACC 120  
 QY 61 ATCTCTCTCAAGGCCAGCCAAAGTGTTCATTATGATGTGTATATATG---TGGTAC 117  
 Db 121 ATCTCTCTCAAGGCCAGCCAAAGTGTTCATTATGATGTGTATATATGAACTGGTAC 180  
 QY 118 CAACAGAAACACGAGACGCCACCAAACTCTCTACCTATGTCATCCATCCAACTCTAGAACT 177  
 Db 181 CAACAGAAACACGAGACGCCACCAAACTCTCTATCTATGTCATCCAACTCTAGAACT 240  
 QY 178 GGGATCCAGCCAGCTTTAGTGGCAGTGGCTGGGACAGACTTCACCCCTCAACATCCAT 237  
 Db 241 GGGATCCAGCCAGCTTTAGTGGCAGTGGCTGGGACAGACTTCACCCCTCAACATCCAT 300  
 QY 238 CTTGTGGAGGAGGAGTGTCTCAACCTATTACTGTCTGCTTTGTAATGAGGATCCCTCC 297  
 Db 301 CTTGTGGAGGAGGAGTGTCTCAACCTATTACTGTCTGCTTTGTAATGAGGATCCCTCC 360  
 QY 298 ACCTTCGGTGTGGACCAAGCTGGAGCTGAAA 330  
 Db 361 ACCTTCGGTGTGGACCAAGCTGGAGCTGAAA 393

RESULT 4  
 BD090651 714 bp DNA linear PAT 27-AUG-2002  
 LOCUS  
 DEFINITION Drug containing humanized anti-Fas antibody.  
 ACCESSION BD090651  
 VERSION BD090651.1 GI:22636261  
 KEYWORDS JP 2001342149-A/2.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 714)  
 AUTHORS Takahashi, W., Haruyama, H. and Serizawa, N.  
 TITLE Drug containing humanized anti-Fas antibody  
 JOURNAL Patent: JP 2001342149-A 2 11-DEC-2001;  
 SANKYO CO LTD

COMMENT  
 OS Mus musculus (mouse)  
 PN JP 2001342149-A/2  
 PD 11-DEC-2001  
 PF 28-MAR-2001  
 PI WATARU TAKAHASHI, HIDEYUKI HARUYAMA, NOBUFUSA SERIZAWA PC  
 A61K39/395, A61K39/395, A61P1/16, A61P7/06, A61P9/00, A61P9/10, PC  
 A61P13/12  
 PC A61P17/00, A61P31/14, A61P31/18, A61P31/20, A61P37/00, A61P37/06,  
 PC A61P37/08,  
 PC A61P43/00/C12N15/02, C12N15/00  
 CC Drug containing humanized anti-Fas antibody  
 FH Key Location/Qualifiers  
 FT CDS (1) . (714)  
 FT mat\_peptide (61) . (714)  
 FT sig\_peptide (1) . (60)

FEATURES  
 source  
 1..714  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 BASE COUNT 200 a 184 c 173 g 157 t  
 ORIGIN

Query Match 88.8%; Score 293; DB 6; Length 714;  
 Best Local Similarity 94.6%; Pred. No. 1.2e-88;  
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;  
 QY 1 GACATTGTGCTCACCACCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGCGAGAGGCCACC 60  
 Db 61 GACATTGTGCTCACCACCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGCGAGAGGCCACC 120  
 QY 61 ATCTCTCTCAAGGCCAGCCAAAGTGTTCATTATGATGTGTATATATG---TGGTAC 117  
 Db 121 ATCTCTCTCAAGGCCAGCCAAAGTGTTCATTATGATGTGTATATATGAACTGGTAC 180  
 QY 118 CAACAGAAACACGAGACGCCACCAAACTCTCTACCTATGTCATCCATCCAACTCTAGAACT 177  
 Db 181 CAACAGAAACACGAGACGCCACCAAACTCTCTATCTATGTCATCCAACTCTAGAACT 240  
 QY 178 GGGATCCAGCCAGCTTTAGTGGCAGTGGCTGGGACAGACTTCACCCCTCAACATCCAT 237  
 Db 241 GGGATCCAGCCAGCTTTAGTGGCAGTGGCTGGGACAGACTTCACCCCTCAACATCCAT 300  
 QY 238 CTTGTGGAGGAGGAGTGTCTCAACCTATTACTGTCTGCTTTGTAATGAGGATCCCTCC 297  
 Db 301 CTTGTGGAGGAGGAGTGTCTCAACCTATTACTGTCTGCTTTGTAATGAGGATCCCTCC 360  
 QY 298 ACCTTCGGTGTGGACCAAGCTGGAGCTGAAA 330  
 Db 361 ACCTTCGGTGTGGACCAAGCTGGAGCTGAAA 393

RESULT 5  
 E40005 714 bp DNA linear PAT 31-JAN-2002  
 LOCUS  
 DEFINITION Drug containing anti-Fas antibody.  
 ACCESSION E40005  
 VERSION E40005.1 GI:18627121  
 KEYWORDS JP 2000169393-A/2.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 714)  
 AUTHORS Serizawa, N., Haruyama, H., Takahashi, W., Yoshida, H., Ichikawa, K.,  
 Okuna, J., Otsuki, M., Shiraishi, A. and Yonehara, S.  
 TITLE Drug containing anti-Fas antibody  
 JOURNAL Patent: JP 2000169393-A 2 20-JUN-2000;  
 SANKYO CO LTD  
 COMMENT  
 OS Mus musculus (mouse)  
 PN JP 2000169393-A/2  
 PD 20-JUN-2000  
 PF 30-SEP-1999 JP 1999278301  
 PR

PI NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, WATARU TAKAHASHI, PI  
 HIROKO YOSHIDA,  
 PI KIMIHIISA ICHIKAWA, JUN OKUMA, MASAHICO OTSUKI, AKIO SHIRAISHI, PI  
 SHIN YONEHARA  
 PC A61K39/395, A61K39/395, A61P1/16, A61P7/06, A61P9/00, PC  
 A61P13/12  
 PC A61P17/00, A61P31/18, A61P37/06, C12N5/10, C12N15/02, C12N15/09, PC  
 C12P21/08//  
 PC C07K16/28, C12N5/00, C12N15/00, C12N15/00  
 CC  
 FH Key Location/Qualifiers  
 FT CDS (1) . (714)  
 FT mat\_peptide (61) . (714)  
 FT sig\_peptide (1) . (60)



79	ATCTCCTGCAAGGCCACGCCAAAGTGTGATTATGATGGTGATAGTTATATGAACTGGTAC	138
118	CAACAGAAAAACGAGACAGCCACCAAACTCCTCACCTATGCTGTCGATCCCAATCTAGAATCT	177
139	CAACAGAAAAACGAGACAGCCACCAAACTCCTCATCTATGCTGCATCCCAATCTAGAATCT	198
178	GGGATCCCAAGCCAGGTTTATGTAGTCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT	237
199	GGGATCCCAAGCCAGGTTTATGTAGTCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT	258
238	CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTACGTTTGTAAAGAGGATCCTGCC	297
259	CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTACGAAAGTAGTGAGGATCCTCCG	318
298	ACGTTCCGTGCTGGGACCAAGCTGGAGCTGAAA	330
319	ACGTTCCGTGAGGACCAAGCTGGAAATCAAA	351

SOURCE	Mus sp.
ORGANISM	Mus sp.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 925)
AUTHORS	Mitsuhashi, O., Takayuki, K. and Ikuno, M.
TITLE	Antibody and nucleic acid encoding the same
JOURNAL	Patent: JP 1999332563-A 3 07-DEC-1999;
COMMENT	ASAHII CHEM IND CO LTD OS Mus sp. (mouse) PN JP 1999332563-A/3 PD 07-DEC-1999 PF 26-MAY-1998 JP 1998163034 PR P1 MITSUHASHI ONO, TAKAYUKI KUSAKA, IKUNO MORIMOTO PC C12N15/02, A61K39/395, A61K39/395, C07K16/28, C12N15/09, C12P21/08

```

FEATURES
  source
    Location/Qualifiers
      1..925
        /organism="Mus sp."
        /mol_type="genomic DNA"
        /db_xref="taxon:10095"
BASE COUNT
  223 a 236 c 268 g 198 t
ORIGIN
  Query Match 88.8%; Score 293; DB 6; Length 925;
  Best Local Similarity 94.8%; Pred. No. 1.2e-88;
  Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1

```

67	GACATTGCTGACCCAAATCTCCAGCTTCTTTGGTGCTCTAGGCGCAGAGGCCACC	126
DB		
61	ATCTCCTGCAAGCCAGCCAAAAGTGTGAATTATGATGGTGATAGTTATATG---	117
QY		
127	ATCTCCTGCAAGCCAGCCAAAAGTGTGAATTATGATGGTGATAGTTATATGCACTGGGTAC	186
DB		
118	CAACAGAAACCAAGSACAGCCACCACCAATCTCCACCTATGCTGCATCCAACTCTAGAAATCT	177
QY		
187	CAACAGAAACCAAGSACAGCCACCACCAATCTCCATCTATGCTGCATCCAACTCTAGAAATCT	246
DB		

```

QY 178 GGGATCCAGCCAGGTTTACTGTCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237
DB 247 GGGATCCAGCCAGGTTTACTGTCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT 306
QY 238 CCTGTGAGGAGGAGGATGCTGCAACTATTACTGTACCTTTGTAATGAGGATCCTCCC 297
DB 307 CCTGTGAGGAGGAGGATGCTGCAACTATTACTGTACCAAGTAGTGAGGATCCTCCG 366
QY 298 ACGTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
DB 367 ACGTTCGGTGGAGGACCAAGCTGGAAATCAAA 399

RESULT 10
LOCUS E30617 925 bp DNA linear PAT 18-JUN-2001
DEFINITION Antibody and nucleic acid encoding the same.
ACCESSION E30617
VERSION E30617.1 GI:13017183
KEYWORDS JP 199332563-A/4.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Mitsuharu, O., Takayuki, K. and Ikuo, M.
COMMENT Antibody and nucleic acid encoding the same
JOURNAL Patent: JP 199332563-A 4 07-DEC-1999;
SAHAI CHEM IND CO LTD
OS Mus sp. (mouse)
PN JP 199332563-A/4
PD 07-DEC-1999
PF 26-MAY-1998 JP 1998163034
PR
PI MITSU HARU ONO, TAKAYUKI KUSAKA, IKUO MORIMOTO
PC C12N15/02, A61K39/395, A61K39/355, C07K16/28, C12N15/09, C12P21/08,
PC C12N15/00,
PC C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..925
FT /organism="Mus sp. (mouse)".
FEATURES
source
Location/Qualifiers
1..925
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
BASE COUNT 223 a 236 c 268 g 198 t
ORIGIN
Query Match 88.8%; Score 293; DB 6; Length 925;
Best Local Similarity 94.6%; Pred. No. 1.2e-88;
Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;
QY 1 GACATTTGCTCACCATTCTCCAGCTTCTTTGGCTGTCTCTAGGCGAGAGGCCACC 60
DB 466 GACATTTGCTCACCATTCTCCAGCTTCTTTGGCTGTCTCTAGGCGAGAGGCCACC 525
QY 61 ATCTCTCTGCAAGGCCAGCCAAAGTGTGATTATGATGGTGTATATG---TGGTAC 117
DB 526 ATCTCTCTGCAAGGCCAGCCAAAGTGTGATTATGATGGTGTATATGATGACTGTATC 585
QY 118 CAACAGAACCCAGGACAGCCCAACCTCTACCTATGCTGCAATCCCAATCTAGATCT 177
DB 586 CAACAGAACCCAGGACAGCCCAACCTCTACCTATGCTGCAATCCCAATCTAGATCT 645
QY 178 GGGATCCAGCCAGGTTTACTGTCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237
DB 646 GGGATCCAGCCAGGTTTACTGTCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT 705
QY 238 CCTGTGAGGAGGAGGATGCTGCAACTATTACTGTACCTTTGTAATGAGGATCCTCCC 297

```

```

DB 705 CCTGTGAGGAGGAGGATGCTGCAACTATTACTGTGCAAAAGTAGTGAGGATCCTCCG 765
QY 298 ACGTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
DB 766 ACGTTCGGTCTGGGACCAAGCTGGAAATCAAA 798

RESULT 11
LOCUS MUSL711GKV 354 bp mRNA linear ROD 29-OCT-1994
DEFINITION Mouse hybridoma Ig rearranged kappa-chain mRNA V-region, partial cds.
ACCESSION M97875
VERSION M97875.1 GI:198677
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Lohman, K.L., Buck, D.W., Carrillo, M.A. and Kennedy, R.C.
COMMENT Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence unpublished, (1992)
JOURNAL Original source text: Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.
FEATURES
source
Location/Qualifiers
1..354
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/map="6"
/tissue_type="SP20-BALB/c fusion hybridoma"
1..354
/gene="Igk"
1..354
/gene="Igk"
/standard_name="L71; monoclonal antibody (CD4 antigen specificity)"
BASE COUNT 92 a 92 c 90 g 80 t
ORIGIN
Query Match 87.8%; Score 289.8; DB 10; Length 354;
Best Local Similarity 94.0%; Pred. No. 1.4e-87;
Matches 313; Conservative 0; Mismatches 17; Indels 3; Gaps 1;
QY 1 GACATTTGCTCACCATTCTCCAGCTTCTTTGGCTGTCTCTAGGCGAGAGGCCACC 60
DB 1 GACATTTGCTGACCCCAATCTCCAGCTTCTTTGGCTGTCTCTAGGCGAGAGGCCACC 60
QY 61 ATCTCTCTGCAAGGCCAGCCAAAGTGTGATTATGATGGTGTATATG---TGGTAC 117
DB 61 ATCTCTCTGCAAGGCCAGCCAAAGTGTGATTATGATGGTGTATATGATGACTGTATC 120
QY 118 CAACAGAACCCAGGACAGCCCAACCTCTACCTATGCTGCAATCCCAATCTAGATCT 177
DB 121 CAACAGAACCCAGGACAGCCCAACCTCTATCTATGCTGCAATCTAGATCT 180
QY 178 GGGATCCAGCCAGGTTTACTGTCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237
DB 181 GGGATCCAGCCAGGTTTACTGTCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT 240
QY 238 CCTGTGAGGAGGAGGATGCTGCAACTATTACTGTACCTTTGTAATGAGGATCCTCCC 297
DB 241 CCTGTGAGGAGGAGGATGCTGCAACTATTACTGTACCAAGTAGTAGGATCCTCCG 300
QY 298 ACGTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330
DB 301 ATGTTTGGAGGGGGACCAAGCTGGAGATATAA 333

```





Qy 238 CCTGTGGAGGAGGAGATGCTGCACCTATTACTGTACGCTTTGTAAATGAGGATCCTCCC 297  
Db |||||  
Qy 241 CCTGTGGAGGAGGAGATGCTGCACCTATTACTGTACGCTTTGTAAATGAGGATCCTCCC 300  
Db |||||

Qy 298 ACGTTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330  
Db |||||

Qy 301 ACGTTTCGGTCTGGGACCAAGCTGGAGCTGAAA 333  
Db |||||

Search completed: January 14, 2004, 17:00:19  
Job time : 1625.9 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 14:23:59 ; Search time 169.524 Seconds  
(without alignments)  
5254.805 Million cell updates/sec

Title: US-09-759-112a-22

Perfect score: 330

Sequence: 1 gacattgtctaccacatcc.....ggaccaagctggagctgaaa 330

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_19Jun03.\*

1:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	330	100.0	330	24	Murine Mab 1F7 lig
2	330	100.0	330	24	Murine Mab 1F7 lig
3	294.6	89.3	396	16	Mouse Mab 3B9 lig
4	294.6	89.3	396	20	Light chain variab
5	294.6	89.3	396	20	Light chain coding
6	293	88.8	333	21	Antibody 4H5 L cha
7	293	88.8	333	21	Murine derived DNA
8	293	88.8	714	19	Anti-Fas Mab HFE7A

9	293	88.8	714	21	AAA72109	cDNA encoding mous
10	293	88.8	714	21	AAA11547	Murine anti-Fas an
11	293	88.8	714	24	ABL45926	Mouse humanised an
12	293	88.8	714	24	ABL48669	Humanised anti-Fas
13	293	88.8	925	21	AAZ59663	Antibody 4H5 H cha
14	293	88.8	925	21	AAZ59664	Antibody 4H5 L cha
15	293	88.8	925	21	AAZ44205	Murine derived DNA
16	293	88.8	925	21	AAZ44206	Murine derived DNA
17	288.2	87.3	333	15	AAQ65554	Mouse anti-HIV mab
18	288.2	87.3	333	15	AAQ70372	Anti HIV antibody
19	286.6	86.8	333	24	ABK88124	DNA encoding mouse
20	286.6	86.8	831	24	AAZ29309	Human penton base
21	286.6	86.8	831	25	ABX12745	DNA encoding mouse
22	285	86.4	334	10	AAZ90492	Gene fragment of i
23	285	86.4	333	14	AAQ35609	Anti-CD4 antibody
24	285	86.4	733	13	AAQ25658	Mouse 0.5beta anti
25	285	86.4	780	10	AAZ90495	A v chi region gen
26	282.4	85.6	669	18	AAZ59338	MHI monoclonal ant
27	280.8	85.1	900	11	AAQ04039	Anti-Leu 3a light
28	277	83.9	336	22	AAZ62145	Anti-SAF-1 monoclo
29	275.4	83.5	768	19	AAV70076	Anti-Fas humanised
30	275.4	83.5	768	21	AAZ72126	DNA encoding human
31	275.4	83.5	768	21	AAA11564	Humanised anti-Fas
32	275.4	83.5	768	24	ABL45943	Humanised anti-Fas
33	275.4	83.5	768	24	ABL48686	Humanised anti-Fas
34	273.8	83.0	309	21	AAZ58662	Antibody 4H5 L cha
35	273.8	83.0	309	21	AAZ44204	Murine derived DNA
36	272.2	82.5	768	19	AAV70075	Anti-Fas humanised
37	272.2	82.5	768	19	AAV70078	Anti-Fas humanised
38	272.2	82.5	768	21	AAZ72125	DNA encoding human
39	272.2	82.5	768	21	AAA72177	DNA encoding human
40	272.2	82.5	768	21	AAA11563	Humanised anti-Fas
41	272.2	82.5	768	21	AAA11615	Humanised HFE7A de
42	272.2	82.5	768	24	ABL45942	Humanised anti-Fas
43	272.2	82.5	768	24	ABL45994	Humanised anti-Fas
44	272.2	82.5	768	24	ABL48685	Humanised anti-Fas
45	272.2	82.5	768	24	ABL48737	Humanised anti-Fas

#### ALIGNMENTS

RESULT 1  
AAL48660  
ID AAL48660 standard; DNA; 330 BP.  
XX  
AC AAL48660;  
XX  
DT 11-OCT-2002 (first entry)  
XX  
DE Murine Mab 1F7 light chain coding sequence.  
XX  
KW Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;  
KW Complementarity determining region; framework-determining region;  
KW FR; heavy chain; light chain; HIV infection; gene; ss.  
XX  
Mus sp.  
XX OS  
XX WO200255568-A2.  
XX  
PD 18-JUL-2002.  
XX  
PF 11-JAN-2002; 2002WO-US00927.  
XX  
PR 11-JAN-2001; 2001US-0759112.  
XX (IMMP-) IMMOPHERON INC.  
XX  
PI Muller S, Kohler H;  
XX  
DR WPI; 2002-590668/63.  
XX  
PT New polynucleotide encoding a complementarity- or framework-determining



PT region of an anti-idiotypic antibody that binds to human or primate  
PT anti- human immunodeficiency virus (HIV) antibodies, for use in  
XX vaccines against HIV  
XX  
PS Claim 10; Page 22-23; 27pp; English.  
XX  
CC The present invention relates to coding sequences of the murine 1F7  
CC anti-idiotypic antibody complementarity-determining region (CDR) or  
CC framework-determining region (FR). The antibody binds to human or primate  
CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the  
CC treatment of HIV infection. The present sequence is the 1F7 light chain  
XX coding sequence.  
XX  
SQ Sequence 330 BP; 80 A; 87 C; 83 G; 80 T; 0 other;  
  
Query Match 100.0%; Score 330; DB 24; Length 330;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GACATTGTGCTACCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
DB 1 GACATTGTGCTACCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
  
QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTATGATGGTGATATATATGTTACCAA 120  
DB 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTATGATGGTGATATATATGTTACCAA 120  
  
QY 121 CAGAAACACGAGCAGCCACCACCAACTCTCATCTGTCATCCCAATCTAGAAATCTGG 180  
DB 121 CAGAAACACGAGCAGCCACCACCAACTCTCATCTGTCATCCCAATCTAGAAATCTGG 180  
  
QY 181 ATCCAGCCAGGTTAGTGCAGTGGTCTGGGACAGACTTCACCTCAACATCCATCT 240  
DB 181 ATCCAGCCAGGTTAGTGCAGTGGTCTGGGACAGACTTCACCTCAACATCCATCT 240  
  
QY 241 GTGAGGAGGAGGATGCTCAACTTACTGTGACGTTTGTAAATGAGGATCTCCACG 300  
DB 241 GTGAGGAGGAGGATGCTCAACTTACTGTGACGTTTGTAAATGAGGATCTCCACG 300  
  
QY 301 TTGGTGTCTGGACCAAGCTGGAGCTGAAA 330  
DB 301 TTGGTGTCTGGACCAAGCTGGAGCTGAAA 330  
  
RESULT 2  
AAL48661  
ID AAL48661 standard; DNA; 330 BP.  
XX  
AC AAL48661;  
XX  
XX 11-OCT-2002 (first entry)  
XX  
DE Murine Mab 1F7 light chain coding sequence.  
XX  
XX  
XX Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR;  
XX complementarity determining region; framework-determining region;  
XX FR; heavy chain; light chain; HIV infection; gene; ss.  
XX  
OS Mus sp.  
XX  
XX Key Location/Qualifiers  
XX CDS 1..330  
XX  
XX /tag= a  
XX /product= "1F7 light chain"  
XX /partial  
XX /note= "no start or stop codon"  
XX  
XX WO200255668-A2.  
XX  
XX 18-JUL-2002.  
XX  
XX 11-JAN-2002; 2002WO-US00927.  
XX  
XX

PR 11-JAN-2001; 2001US-0759112.  
XX (IMMP-) IMMOPHERON INC.  
XX  
XX Muller S, Kohler H;  
XX  
XX WPI; 2002-590668/63.  
XX P-PSDB; AAO18536.  
XX  
XX New polynucleotide encoding a complementarity- or framework-determining  
XX region of an anti-idiotypic antibody that binds to human or primate  
XX anti- human immunodeficiency virus (HIV) antibodies, for use in  
XX vaccines against HIV  
XX  
PS Disclosure; Page 23; 27pp; English.  
XX  
CC The present invention relates to coding sequences of the murine 1F7  
XX anti-idiotypic antibody complementarity-determining region (CDR) or  
XX framework-determining region (FR). The antibody binds to human or primate  
XX anti-human immunodeficiency virus (HIV) antibodies and can be used in the  
XX treatment of HIV infection. The present sequence is the 1F7 light chain  
XX coding sequence.  
XX  
SQ Sequence 330 BP; 80 A; 87 C; 83 G; 80 T; 0 other;  
  
Query Match 100.0%; Score 330; DB 24; Length 330;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GACATTGTGCTACCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
DB 1 GACATTGTGCTACCAATCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
  
QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTATGATGGTGATATATATGTTACCAA 120  
DB 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTATGATGGTGATATATATGTTACCAA 120  
  
QY 121 CAGAAACACGAGCAGCCACCACCAACTCTCATCTGTCATCCCAATCTAGAAATCTGG 180  
DB 121 CAGAAACACGAGCAGCCACCACCAACTCTCATCTGTCATCCCAATCTAGAAATCTGG 180  
  
QY 181 ATCCAGCCAGGTTAGTGCAGTGGTCTGGGACAGACTTCACCTCAACATCCATCT 240  
DB 181 ATCCAGCCAGGTTAGTGCAGTGGTCTGGGACAGACTTCACCTCAACATCCATCT 240  
  
QY 241 GTGAGGAGGAGGATGCTCAACTTACTGTGACGTTTGTAAATGAGGATCTCCACG 300  
DB 241 GTGAGGAGGAGGATGCTCAACTTACTGTGACGTTTGTAAATGAGGATCTCCACG 300  
  
QY 301 TTGGTGTCTGGACCAAGCTGGAGCTGAAA 330  
DB 301 TTGGTGTCTGGACCAAGCTGGAGCTGAAA 330  
  
RESULT 3  
AAQ83490  
ID AAQ83490 standard; cDNA; 396 BP.  
XX  
XX AAQ83490;  
XX  
XX 25-MAR-2003 (updated)  
XX 20-SEP-1995 (first entry)  
XX  
XX Mouse Mab 3B9 light chain.  
XX  
XX Chimeric antibody; humanized antibody; antibody engineering;  
XX monoclonal antibody; Mab; interleukin-4; IL-4; allergy; ds.  
XX  
XX Mus sp.  
XX  
XX Key Location/Qualifiers  
XX CDS 1..396  
XX  
XX /\*tag= a  
XX





QY 238 CCTGTGGAGGAGAGATGCTCAACCTATTACTCTCAGCTTTGTAATGAGATCCTCCC 297  
 Db 241 CCTGTGGAGGAGAGATGCTCAACCTATTACTCTCAGCTTTGTAATGAGATCCTCCC 300

QY 298 AGCTTCGGTGGTGGGACCAAGCTGGAGCTGAAA 330  
 Db 301 AGCTTCGGTGGGAGGACCAAGCTGGAAATCAAA 333

## RESULT 7

AAZ44232

ID AAZ44232 standard; DNA; 333 BP.

XX

AC AAZ44232;

XX

DT 31-MAR-2000 (first entry)

XX

DE Murine derived DNA fragment #6.

XX

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine; ds.

XX

OS Mus sp.

XX

FN WO9961629-A1.

XX

PD 02-DEC-1999.

XX

PF 24-MAY-1999; 99WO-JP02711.

XX

PR 25-MAY-1998; 98JP-0159957.

XX

PR 26-MAY-1998; 98JP-0163023.

XX

PA (ASAH ) ASARI KASEI KOGYO KK.

XX

PA (ASAH ) ASARI MEDICAL CO LTD.

XX

FI Ono M, Soka T, Morimoto I, Miyamura K;

XX

DR WPI; 2000-086720/07.

XX

DR P-PSDB; AAV51146.

XX

PT Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -

XX

PS Disclosure; Page 97-98; 11pp; Japanese.

XX

CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence encodes a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.

XX

SQ Sequence 333 BP; 87 A; 86 C; 84 G; 76 T; 0 other;

XX

Query Match 88.8%; Score 293; DB 21; Length 333;

XX

Best Local Similarity 94.6%; Pred. No. 6.6e-81;

XX

Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

XX

QY 1 GACATTGTGCTCACCAATTCACGTTCTTTGGTGTCTCTTAGGGCAGAGGCCACC 60

Db

1 GACATTGTGCTGACCAATTCACGTTCTTTGGTGTCTCTTAGGGCAGAGGCCACC 60

XX

QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTATGATGGTGATAGTTATATG---TGSTAC 117

XX

61 ATCTCTGCAAGCCAGCCAAAGTGTGATTATGATGGTGATAGTTATATGAACTGGTAC 120

Db

QY 118 CAACAGAAACAGGACAGCCACCAACTCTCTCAGCTATCTGATCCATCTAGAAATCT 177  
 Db 121 CAACAGAAACAGGACAGCCACCAACTCTCTCAGCTATCTGATCCATCTAGAAATCT 180  
 QY 178 GGGATCCAGCCAGGTTTGTAGTGGCAGTGGGTCTGGGACAGACTTCCACCTCAACATCCAT 237  
 Db 181 GGGATCCAGCCAGGTTTGTAGTGGCAGTGGGTCTGGGACAGACTTCCACCTCAACATCCAT 240  
 QY 238 CCTGTGGAGGAGGAGTGTCTGCAACTATTATCTGTCAGCTTTGTAATGAGGATCCTCCC 297  
 Db 241 CCTGTGGAGGAGGAGTGTCTGCAACTATTATCTGTCAGCAAAAGTAGTGAGGATCCTCCG 300  
 QY 298 ACCTTCGGTGTGGGACCAAGCTGGAGCTGAAA 330  
 Db 301 ACCTTCGGTGTGGGACCAAGCTGGAAATCAAA 333

## RESULT 8

AAV70130

ID AAV70130 standard; cDNA to mRNA; 714 BP.

XX

AC AAV70130;

XX

DT 25-MAR-2003 (updated)

XX

DT 15-MAR-1999 (first entry)

XX

DE Anti-Fas MAb HPE7A light chain cDNA.

XX

KW HPE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HPE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy; ds.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

XX

FT sig\_peptide 1..60

XX

FT mat\_peptide 61..714

XX

FT mat\_peptide /\*tag= b

XX

XX AU9859701-A.

XX

XX 08-OCT-1998.

XX

XX 30-MAR-1998; 98AU-0059701.

XX

XX 08-OCT-1997; 97JP-0276064.

XX

XX 01-APR-1997; 97JP-0082953.

XX

XX 25-JUN-1997; 97JP-0169088.

XX

XX (SANY ) SANKYO CO LTD.

XX

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX

XX Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX

XX WPI; 1998-543440/01.

XX

XX P-PSDB; AAW83042.

XX

XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 XX used to evaluate drugs in animal models and to treat Fas-associated  
 XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 XX myocarditis, hepatitis and AIDS

XX

PS Reference Example 4; Page 188-189; 292pp; English.

CC This nucleotide sequence codes for the light chain (see AAWS3042) of  
 CC murine anti-human Fas monoclonal antibody HFE7A. The cDNA was  
 CC obtained from HFE7A-secreting hybridoma cells (FERM BP-5828) by  
 CC RT-PCR (see AAU70127-28). The invention provides humanised versions  
 CC of HFE7A (see AAWS3031-37) which, like HFE7A, are capable of inducing  
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting  
 CC Fas-induced apoptosis in normal cells. The humanised antibodies  
 CC are used to evaluate, in animal models, treatments of diseases that  
 CC involve Fas/Fas ligand interactions, and also to treat such  
 CC diseases, including autoimmune disease (e.g. systemic lupus  
 CC erythematosus, Hashimoto's disease, graft versus host disease,  
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,  
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid  
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia  
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura  
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
 CC (Updated on 25-MAR-2003 to correct DR field.)  
 XX  
 SQ Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;  
 Query Match 88.8%; Score 293; DB 19; Length 714;  
 Best Local Similarity 94.6%; Pred. No. 8.5e-81;  
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;  
 QY 1 GACATTGTGCTCACCACCAATCTCCAGCTTCTTTGGGTGTCTCTAGGCGAGAGGCCACC 60  
 Db 61 GACATTGTGCTGACCCCAATCTCCAGCTTCTTTGGGTGTCTCTAGGCGAGAGGCCACC 120  
 QY 61 ATCTCTCTCAGGCGAGAGGTGTTGATTATGATGTTGATGTTATATG---TGGTAC 117  
 Db 121 ATCTCTCTCAGGCGAGAGGTGTTGATTATGATGTTGATGTTATATGATGTTATGTTATG 180  
 QY 118 CAACAGAAACACGAGCAGCCACCACTCTCTACCTATGTCATCCAACTAGAAATCT 177  
 Db 181 CAACAGAAACACGAGCAGCCACCACTCTCTACCTATGTCATCCAACTAGAAATCT 240  
 QY 178 GGGATCCCGAGGAGGAGTGTAGTGGCAGTGTGATGTTGATGTTGATGTTATGTTATGTTATG 237  
 Db 241 GGGATCCCGAGGAGGAGTGTAGTGGCAGTGTGATGTTGATGTTGATGTTATGTTATGTTATG 300  
 QY 238 CCGTGGGTGCTGGGACCAAGCTGGAGCTGAAA 330  
 Db 361 ACGTTCGGTGGAGGACCAAGCTGGAATCAAA 393  
 RESULT 9  
 AAU72109  
 ID AAA72109 standard; cDNA; 714 BP.  
 AC AAA72109;  
 XX  
 XX 24-NOV-2000 (first entry)  
 DT  
 DE CDNA encoding mouse anti-Fas antibody HFE7A light chain.  
 XX  
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; complementarity determining region; CDR; human Fas;  
 KW Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancyelophthisis;  
 KW hepatitis; AIDS; graft rejection; light chain; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN JP2000169393-A.  
 XX  
 XX 20-JUN-2000.

XX 30-SEP-1999; 99JP-0278301.  
 XX PF  
 XX 30-SEP-1998; 98JP-0278883.  
 XX PR  
 XX (SANY ) SANKYO CO LTD.  
 XX PA  
 XX WPI; 2000-485645/43.  
 XX DR P-PSDB; AAB14748.  
 XX DR  
 XX Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 XX  
 XX Example 4; Page 69-70; 139pp; Japanese.  
 XX  
 XX The invention relates to compositions for the prevention or treatment  
 CC or diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs  
 CC (complementarity determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The composition of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. The present sequence represents cDNA  
 CC encoding the light chain of the murine anti-human Fas monoclonal  
 CC antibody HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).  
 XX  
 SQ Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;  
 Query Match 88.8%; Score 293; DB 21; Length 714;  
 Best Local Similarity 94.6%; Pred. No. 8.5e-81;  
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;  
 QY 1 GACATTGTGCTCACCACCAATCTCCAGCTTCTTTGGGTGTCTCTAGGCGAGAGGCCACC 60  
 Db 61 GACATTGTGCTGACCCCAATCTCCAGCTTCTTTGGGTGTCTCTAGGCGAGAGGCCACC 120  
 QY 61 ATCTCTCTCAGGCGAGCAGCCAAAGTGTGATTATGATGTTGATGTTATGTTATGTTATGTTATG 117  
 Db 121 ATCTCTCTCAGGCGAGCAGCCAAAGTGTGATTATGATGTTGATGTTATGTTATGTTATGTTATG 180  
 QY 118 CAACAGAAACACGAGCAGCCACCACTCTCTACCTATGTCATCCAACTAGAAATCT 177  
 Db 181 CAACAGAAACACGAGCAGCCACCACTCTCTACCTATGTCATCCAACTAGAAATCT 240  
 QY 178 GGGATCCCGAGGAGTGTAGTGGCAGTGTGATGTTGATGTTGATGTTATGTTATGTTATGTTATG 237  
 Db 241 GGGATCCCGAGGAGTGTAGTGGCAGTGTGATGTTGATGTTGATGTTATGTTATGTTATGTTATG 300  
 QY 238 CCGTGGGTGCTGGGACCAAGCTGGAGCTGAAA 330  
 Db 361 ACGTTCGGTGGAGGACCAAGCTGGAATCAAA 393  
 RESULT 10  
 AAU1547  
 ID AAU1547 standard; cDNA; 714 BP.  
 AC AAU1547;  
 XX  
 XX 08-AUG-2000 (first entry)  
 DT  
 DE Murine anti-Fas antibody HFE7A light chain cDNA.  
 XX  
 XX Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;

KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.  
 XX Mus musculus.  
 XX  
 XX EP990663-A2.  
 XX  
 XX 05-APR-2000.  
 XX  
 XX 29-SEP-1999; 99EP-0307711.  
 XX  
 XX 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 XX  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WPI; 2000-258930/23.  
 DR P-PSDB; AAW90898.  
 XX

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX  
 XX Example reference 4; Page 102-103; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence encodes  
 CC a murine anti-Fas monoclonal antibody HFE7A light chain described in the  
 CC method of the invention.

XX Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;  
 SQ  
 Query Match 88.8%; Score 293; DB 21; Length 714;  
 Best Local Similarity 94.6%; Pred. No. 8.5e-81;  
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 1 GACATTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
 DB  
 61 GACATTGCTCAGCCCAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 120

QY 61 ATCTCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGTATATG---TGGTAC 117  
 DB 121 ATCTCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGTATATGAACTGGTAC 180  
 QY 118 CAACAGAAACCCAGGACAGCCACCAAACTCCTCACTATCTGTCATCCCAATCTAGAATCT 177  
 DB 181 CAACAGAAACCCAGGACAGCCACCAAACTCCTCATCTATGTCATCCCAATCTAGAATCT 240  
 QY 178 GGGATCCCGACGAGTGTAGTGGCAGTGGCTCTGGGACAGACTTCACCCCTCAACATCCAT 237  
 DB 241 GGGATCCCGACGAGTGTAGTGGCAGTGGCTCTGGGACAGACTTCACCCCTCAACATCCAT 300  
 QY 238 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTGTCAGCTTTGTATGAGGATCCTCCC 297  
 DB 301 CCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTGTCAGCAAGTATGAGGATCCTCGG 360  
 QY 298 ACGTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330  
 DB 361 ACGTTCGGTGGAGGACCAAGCTGGAATCAAA 393

## RESULT 11

ABL45926  
 ID ABL45926 standard; cDNA; 714 BP.

XX ABL45926;

AC ABL45926;

DT 26-APR-2002 (first entry)

XX Mouse humanised anti-Fas antibody related cDNA SEQ ID NO 8.  
 DE Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;  
 KW light chain subunit; apoptosis; immunosuppressive; antiallergic;  
 KW autoimmune disease; allergy; atopic; ss.

XX Mus musculus.

XX JP2001342148-A.

XX 11-DEC-2001.

XX 28-MAR-2001; 2001JP-0093106.

XX 29-MAR-2000; 2000JP-0090918.

XX (SANY ) SANKYO CO LTD.

XX WPI; 2002-145113/19.

DR P-PSDB; ABB74904.

PT Drug containing humanised anti-Fas antibody, used for preventing and  
 PT treating autoimmune diseases, allergy, and atopy -

XX Example 4 (Preparatory); Page 77-79; 194pp; Japanese.

XX The invention relates to a preventive or treating agent for diseases  
 CC caused by abnormality in Fas/Fas ligand system containing as the active  
 CC component an antibody having as the light chain subunit a polypeptide  
 CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,  
 CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all  
 CC fully defined in the specification and having an activity of combining  
 CC specifically with mammalian Fas and an activity of inducing apoptosis  
 CC in a cell expressing Fas. The agent has immunosuppressive and  
 CC antiallergic activity and is used for preventing and treating autoimmune  
 CC diseases, allergy, atopy and others.

XX Sequence 714 BP; 200 A; 184 C; 173 G; 157 T; 0 other;

Query Match 88.8%; Score 293; DB 24; Length 714;  
 Best Local Similarity 94.6%; Pred. No. 8.5e-81;  
 Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 1 GACATTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60









GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 15:52:50 ; Search time 1328.1 Seconds  
(without alignments)  
6039.083 Million cell updates/sec

Title: US-09-759-112a-22  
Perfect score: 330  
Sequence: 1 gacattggtcaccattc.....ggaccagctggagctgaaa 330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

EST.\*

1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_htc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rtd.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250.4	75.9	659	10	BF137298
2	249.8	75.7	407	10	AW988429
3	245	74.2	683	11	AF240172
4	245	74.2	1108	12	BG969221

5	244.8	74.2	774	10	BF581989
6	244	73.9	750	12	BG965050
7	241.8	73.3	398	9	AA423447
8	241.8	73.3	643	14	BY733441
9	240.4	72.8	831	12	BG966589
10	239.6	72.6	402	9	AI549800
11	239.2	72.5	327	10	BG148320
12	239.2	72.5	876	12	BI107286
13	238.6	72.3	735	12	BG967206
14	238.6	72.3	865	12	BI659552
15	238	72.1	420	9	AI120005
16	237.6	72.0	732	12	BG962768
17	235.4	71.3	806	12	BI108506
18	232.2	70.4	1063	10	BF577971
19	224.2	67.9	922	10	BF584560
20	216	65.5	974	10	BF577946
21	207	62.7	286	10	BG144775
22	201.6	61.1	339	9	AA710249
23	200.4	60.7	266	10	BG145361
24	199.4	60.4	344	13	BY214260
25	198.6	60.2	577	28	AZ942606
26	175.4	53.2	671	11	AF240168
27	174.2	52.8	268	10	BG148476
28	171.2	51.9	756	28	BH054133
29	169.8	51.5	757	10	BG484518
30	164.4	49.8	465	9	AW404697
31	164.4	49.8	727	14	CB956193
32	163.8	49.6	798	10	BG426036
33	162.2	49.2	776	14	CB959429
34	161.2	48.8	755	14	CB957520
35	160.6	48.7	533	9	AW802126
36	160.6	48.7	717	14	CB957784
37	160.6	48.7	777	14	CB957974
38	160.6	48.7	779	14	CB986877
39	160.6	48.7	795	14	CB986276
40	160.6	48.7	889	14	CB985667
41	160.4	48.6	434	9	AW406486
42	160.2	48.5	808	14	CB984840
43	159.6	48.4	482	9	AV733856
44	159.6	48.4	519	9	AW405183
45	159.6	48.4	744	14	CB956406

#### ALIGNMENTS

RESULT 1  
BF137298  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BF137298 601781658F1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4009670 5', mRNA linear EST 24-OCT-2000  
mRNA sequence.

BF137298.1 GI:10976338

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NIH-MGC http://mgi.nci.nih.gov/.

1 (bases 1 to 659)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM9246 row: c column: 15

High quality sequence stop: 657.



(2001)  
 REFERENCE 3 (bases 1 to 683)  
 AUTHORS Qui D., Zeng, G., Yan, X., Wang, F., Tian, F., Ren, D., Zhao, T., Li, X.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-MAR-2000) Molecular Cloning Laboratory, Institute of Genetic Diagnosis, Fourth Military Medical University, No. 17 Chang Le West Road, Xi'an 710032, China  
 FEATURES  
 Location/Qualifiers  
 source  
 1..683  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="BALB/c"  
 /db\_xref="taxon:10090"  
 /sex="male"  
 /cell\_type="intestinal gland cell"  
 /note="derived from differential display PCR between irradiated mice with and without RNA injection"  
 CDS  
 1..352  
 /note="related to the repair of irradiation-damaged intestinal gland cells treated with RNA"  
 /codon\_start=2  
 /product="MRP9"  
 /protein\_id="AAK43734.1"  
 /db\_xref="GI:13877294"  
 /translation="LCGRFORIRIRHRTGCRFFQLQGPSPSRVRLTLVTEIHCRIILHRIYEAIBICRPTASKPGRDPSGLGCSIDEEFWLSEFLFVHKTNANII NTFAGSAGGGPLP"  
 BASE COUNT 153 a 199 c 167 g 163 t 1 others  
 ORIGIN  
 Query Match 74.2%; Score 245; DB 11; Length 683;  
 Best Local Similarity 85.6%; Pred. No. 8e-62; Indels 3; Gaps 1;  
 Matches 285; Conservative 0; Mismatches 45; Indels 3; Gaps 1;  
 QY 1 GACATTGTGCTCACCATTCTCCAGTCTTTGGCTGTCTTAGGGCAGAGGCCAC 60  
 Db 394 GACATCGTGTCTCACCAGTCTCCAGTCTTTGGCTGTCTTAGGGCAGAGGCCAC 335  
 QY 61 ATCTCTGAGGCGCAGCCAAAGTGTGATTATGATGTTGATGTTATG---TGGTAC 117  
 Db 334 ATCTCTGAGGCGCAGCCAAAGTGTGATTATGATGTTGATGTTATG---TGGTAC 275  
 QY 118 CAACAGAACACGAGCAGCCACCAACTCTCTACCTATGCTGCATCCAACTAGATCT 177  
 Db 274 CAGCAGAACACGAGCAGCCACCAACTCTCTATCTATGCTGCATCCAACTAGATCT 215  
 QY 178 GGGATCCCGCAGGTTTGTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237  
 Db 214 GGGGTCCCTGCGCAGTCTTACTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATATAT 155  
 QY 238 CCTGTGGAGGAGGATGCTGCACCTATTACTGTGAGCTTTGTAAATGAGATCCCTCC 297  
 Db 154 CTTATGGAGGAGGATGATCTTCAGTGTATTTCTGCACCAAGTAAAGGAGTTCCTTAC 95  
 QY 298 AGTTTCGTGTCTGGGACCAAGCTGGAGCTGAAA 330  
 Db 94 ACGTTCGGAGGGGGACCAAGCTGGAGCTGAAA 62  
 RESULT 4  
 BG969221  
 LOCUS 602835202F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4989625 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG969221  
 VERSION BG969221.1 GI:14356858  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1108)

NIH-MGC <http://mgc.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM11004 row: c column: 02  
 High quality sequence stop: 508.  
 Location/Qualifiers  
 source  
 1..1108  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4989625"  
 /lab\_host="NCI CGAP Co24"  
 /clone\_lib="NCI CGAP Co24"  
 /notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
 BASE COUNT 286 a 417 c 244 g 161 t  
 ORIGIN  
 Query Match 74.2%; Score 245; DB 12; Length 1108;  
 Best Local Similarity 93.5%; Pred. No. 1.1e-61; Indels 5; Gaps 3;  
 Matches 289; Conservative 0; Mismatches 15; Indels 5; Gaps 3;  
 QY 1 GACATTGTGCTCACCATTCTCCAGTCTTTGGCTGTCTTAGGGCAGAGGCCAC 60  
 Db 63 GACATTGTGCTCACCATTCTCCAGTCTTTGGCTGTCTTAGGGCAGAGGCCAC 122  
 QY 61 ATCTCTGAGGCGCAGCCAAAGTGTGATTATGATGTTGATGTTATG---TGGTAC 117  
 Db 123 ATCTCTGAGGCGCAGCCAAAGTGTGATTATGATGTTGATGTTATG---TGGTAC 182  
 QY 118 CAAC-AGAACACGAGCAGCCACCAACTCTCTACCTATGCTGCATCCAACTAGATC 176  
 Db 183 CAAC-AGAACACGAGCAGCCACCAACTCTCTATCTATGCTGCATCCAACTAGATC 242  
 QY 177 TGGGATCCCGCAGGTTTGTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCA 236  
 Db 243 TGGGATCCCGCAGGTTTGTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCA 302  
 QY 237 TCCTGTGGAGGAGGATGCTGCACCTATTACTGTGAGC-TTTGTAAATGAGATCCTC 295  
 Db 303 CCTGTGGAGGAGGAGGATGCTGCAGCTTATTACTGTGACCAACAGTAAATGAGATCCGT 362  
 QY 296 CCACGTTTCG 304  
 Db 363 ACACGTTTCG 371  
 RESULT 5  
 BF581989  
 LOCUS 602099444F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4219426 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF581989  
 VERSION BF581989.1 GI:11655610  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 774)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

Unpublished

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10989 row: 5 column: 03  
High quality sequence stop: 748.

```

1. .750
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4983962"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 Kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
202 a 193 c 174 t

```

[illegible]

AA423447 398 bp mRNA linear EST 16-OCT-1997  
 ve80a03.r1 Soares mammary gland NDMWG Mus musculus cDNA clone  
 IMAGE:832492 5', similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III  
 REGION (HUMAN); gb:M35669 Mouse Ig aberrantly rearranged  
 kappa-chain mRNA V-J2-C-region, (MOUSE);, mRNA sequence.  
 AA423447  
 AA423447  
 AA423447.1 GI:2102360  
 EST.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 1 (bases 1 to 398)  
 Marra-Ma, Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geissel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished

Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mousees@wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

MGI:492708

Seq primer: -28ml3 rev2 ET from Amersham.

## FEATURES

Location/Qualifiers

1..398

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:832492"

/sex="male"

/tissue\_type="mammary gland"

/dev\_stage="4 weeks"

/lab\_host="DH103"

/clone\_lib="Soares mammary gland NBMWG"

/notes="Organ: mammary gland; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']

TGTTACCAATCGAATGGAGCGCCGCCGATGTTTTTTTTTTTTTTTTTTT

T 3'); double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified p773 vector.

RNA provided by Dr. Minoru Ko, Wayne State Univ. Library

constructed and normalized by Bento Soares and M. Fatima

Bonaldo."

BASE COUNT 101 a 100 c 102 g 95 t

ORIGIN

Query Match 73.3%; Score 241.8; DB 9; Length 398;

Best Local Similarity 85.0%; Pred. No. 5.2e-61;

Matches 283; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 1 GACATTGTGCTACCAATTCCTCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60

66 GACATTGTGCTGACCAATCTCCAGCTTCCTTGGCTGTCTCTAGGGCAGAGGCCACC 125

QY 61 ATCTCTGCAAGCCAGCCAGGCTGTGATTATGATGGTGAATATATG---TGGTAC 117

126 ATCTCTGCAAGCCAGCCAGGCTGTGATTATGATGGTGAATATATG---TGGTAC 185

QY 118 CACAGAAACCCAGGACAGCCACCACCAACCTCCATCTGCTGCATCCAACTAGAACT 177

186 CACAGAAACCCAGGACAGCCACCACCAACCTCCATCTGCTGCATCCAAACAGATCC 245

QY 178 GGGATCCAGCCAGGTTTATGTCAGTGGTCTGGGACAGATTCACCTCCAACTCCAT 237

246 GGGGTCCTCCGCCAGGTTTATGTCAGTGGTCTGGGACAGATTCACCTCCAACTCCAT 305

QY 238 CTTGTGGAGGAGGAGATGCTGCAACTATTACTGTGACCTTTGTAATGAGATCCTCC 297

306 CTTATGAGAGGAGATGATCACTATGATTTCTGTGACCAAGTAGAGATTCCTCGG 365

QY 298 AGTTCCGTCGTCGGGACCAAGCTGGAGCTGAAA 230

366 AGTTCCGTCGTCGGGACCAAGCTGGAGCTGAAA 398

RESULT 8

BY733441

LOCUS

DEFINITION

BY733441.1 RIKEN full-length enriched, adult male accessory axillary lymph node Mus musculus cDNA clone G630004k22 5', mRNA sequence.

BY733441

EST.

BY733441.1 GI:27146568

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 643)

## REFERENCE

## AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, T., Osato, N., Saito, R., Suzuki, H., Yamahata, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, D. J., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, J. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hata, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, Z. and Hayashizaki, Y.

## TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

12466851

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-resgsc.riken.go.jp

URL: <http://genome.gsc.riken.go.jp/>

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda

S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, P., Imotani, K.,

Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno

H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K.,

Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H.,

Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y.,

Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct

Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken



This read has been verified (found to hit its original self in the correct orientation)

Seq primer: -40RP from Gibco.

## FEATURES

```

1. 402
source
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:832492"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NbMMG"
/note="Organ: mammary gland; Vector: pP773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco R1; 1st strand cDNA was primed with a Not 1 - oligo(dT) primer [5].
TGTTACCAATCTGAATGGAGCGCGCGAATGGTTTTTTTTTTTTTTTTTTTTTTT
t 3'; double-stranded cDNA was ligated to Eco R1 adaptors (Pharmacia), digested with Not 1 and cloned into the Not 1 and Eco R1 sites of the modified pP773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

```

BASE COUNT	102 a	101 c	105 g	94 t
ORIGIN				

Query Match	72.6%;	Score	239.6;	DB	9;	Length	402;
Best Local Similarity	85.6%;	Pred. No.	2.4e-60;				
Matches	279;	Conservative	0;	Mismatches	44;	Indels	3;
						Gaps	1;
<hr/>							
QY	1	GACATTTGCTCAACCAATCTCCAGCTCTCTTGGCTGTCTCTAGGCGAGAGGCCACC	60				
Db	66	GACATTTGCTGACCCCAATCTCCAGCTCTCTTGGCTGTCTCTAGGCGAGAGGCCACC	125				
<hr/>							
QY	61	ATCTCTCTCAAGGCCAGCAAAAGTTGATTATGATGGTGATAGTTATATG---	117				
Db	126	ATCTCTCTCAGAGCCAGGAAGTGTGATAATCTTGGCATTAGTTTATGACTGGTTC	185				
<hr/>							
QY	118	CAACAGAAACAGGACAGCCACCCAACTCCTCACTATGCTGCATPCCAATCTAGAATCT	177				
Db	186	CAACAGAAACAGGACAGGCACCCAACTCCTCATCTATGCTGCATCCAAACAAAGATCC	245				
<hr/>							
QY	178	GGGATCCAGCCAGGTTTATGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT	237				
Db	246	GGGGTCCCTGCCAGTTTAGTGGCAGTGGGTCTGGGACAGACTTCAGGCTCAACATCCAT	305				
<hr/>							
QY	238	CTGTGGAGGAGGAGTGTGCAACCTATTATGTCACTTTGTAAATGAGGATCCTCC	297				
Db	306	CCTATGGAGGAGGATGATACTCAATGTAATTTCTGTACGAAAGTAAAGGAGTTCCTCG	365				
<hr/>							
QY	298	ACGTTCTGGTCTGGGACCAAGCTGGA	323				
Db	366	ACGTTCTGGTGGAGGCACCAAGGTGA	391				

RESULT 11  
 BG148320  
 LOCUS  
 DEFINITION  
 u091c06.v1 Soares mouse NMGb bcell Mus musculus cDNA clone  
 IMAGE:3383818 5', similar to SW:KV3H MOUSE P0160 IG KAPPA CHAIN  
 V-III REGION PC 3741/TEPC 111.1; mRNA sequence.  
 BG148320  
 BG148320.1 GI:12651742  
 EST.  
 Mus musculus (house mouse)  
 Mus musculus  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 327)  
 NC1-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 REFERENCE  
 AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbg-remail.nih.gov  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info:image.llnl.gov) for further information.  
MGI:1088814

## FEATURES

```

location/Qualifiers
1. .327
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_image="338318"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares mouse NMGB bcell"
/note="Organ: germinal B-cell; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1:
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTTCACCATCTGAGTGGAGCGCGCGCTGTTTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized; constructed by Bento Soares and
M.Fatima Bonaldo."
83 a 84 c 82 g 78 t

```

BASE COUNT	83 a	84 c	82 g	78 t
ORIGIN				
Query Match	72.5%;	Score 239.2;	DB 10;	Length 327;
Best Local Similarity	85.8%;	Pred. No. 2.8e-60;		
Matches 278;	Conservative 0;	Mismatches 43;	Indels 3;	Gaps 1;
QY	10	CTCACCAATCTCCAGCTCTTTGGCTGTCTCTTAGGGCAGAGGGCCACCATCTCCTGC	69	
Db	1	CTGACCCAACTCCAGCTCTTTGGCTGTCTCTTAGGGCAGAGGGCCACCATATCTCTGC	60	
QY	70	AAGGGCAGCCAAAGTGTTCATTATGATGTGTGATAGTTATATG---TGGTACCAACAGAAA	126	
Db	61	AGAGCCAGTGAAGAGTGTTCATAGTTATGTGCAATAGTTTTATGCACCTGTTACCAAGCAGAAA	120	
QY	127	CCAGGACAGCCACCCAACTCTCCACCTATGCTGCATCCAACTAGAAATCTGGGATCCCA	186	
Db	121	CCAGGACAGCCACCCAAACTCTCTCATCTATCGTGTGCATCCAACTAGAAATCTGGGATCCCT	180	
QY	187	GCACGTTTTAGTGGCAGTGGGTCTGGGACAGACATTCACCCCTCAAATCCATCCTGTGGAG	246	
Db	181	GCACGTTTCAGTGGCAGTGGGTCTTAGGACAGACTTCACCCCTCACCAATTAATCTGTGGAG	240	
QY	247	GAGGAGGATGTGCCAACCTATTACTGTGAGCTTTGTATGAGGATCTCTCCACGTTTCGGT	306	
Db	241	GCTGATGATGTTGCAACCTATTACTGTGTAGCAAAAGTATGAGGATCCGTGGAGCTTCGGT	300	
QY	307	GCTGGGACCAAGCTGGAGCTGAAA	330	
Db	301	GGAGGCTCCAGCTGGAAATCAAA	324	

RESULT 12	
BIL107286	
LOCUS	mRNA linear EST 26-JUN-2001
DEFINITION	602894285F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:503925 5',
ACCESSION	BIL107286 mRNA 876 bp
VERSION	BIL107286.1 GI:14558179 Mus musculus cDNA clone IMAGE:503925 5',
KEYWORDS	mRNA sequence.
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
	1 (bases 1 to 876)
	NIH-MGC http://mgc.nci.nih.gov/.







Db 302 CCTATGGAGGAGGATGATTCTGCAATGTATTTCTGTCAAGTAAGGAGGTTCTTTGG 361  
QY 298 ACGTTCGGTCTGCTGGGACCAAGCTGGA 323  
Db 362 ACGTTCGGTGGAGGCACGAGCTGGA 387

Search completed: January 14, 2004, 17:46:56  
Job time : 1335.6 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 15:55:45 ; Search time 40 Seconds  
(without alignments)  
3641.411 Million cell updates/sec

Title: US-09-759-112A-22  
Perfect score: 330  
Sequence: 1 gacattggtcaccattc.....ggaccagctggagctgaaa 330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTCUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294.6	89.3	396	2	US-08-483-636-1
2	294.6	89.3	396	2	US-08-483-632-1
3	286.6	86.8	333	1	US-08-491-845-7
4	283.4	85.9	393	3	US-08-579-378A-13
5	262.6	79.6	393	1	US-08-137-117D-32
6	262.6	79.6	393	1	US-08-436-717-32
7	261	79.1	333	1	US-08-275-053-10
8	261	79.1	333	1	US-08-275-053-16
9	261	79.1	363	1	US-08-111-080-21
10	261	79.1	363	1	US-08-211-980-21
11	261	79.1	363	5	PCT-US93-07367-21
12	257.8	78.1	339	2	US-08-553-497A-9
13	257.8	78.1	363	1	US-08-111-080-17
14	257.8	78.1	363	1	US-08-111-980-17
15	257.8	78.1	363	5	PCT-US92-07111-16
16	257.8	78.1	363	5	PCT-US93-07367-17
17	254.6	77.2	339	2	US-08-553-497A-5
18	249.8	75.7	393	1	US-07-634-278-66
19	249.8	75.7	393	1	US-08-477-728-66
20	249.8	75.7	393	1	US-08-474-040-66
21	249.8	75.7	393	1	US-08-487-200-66
22	249.8	75.7	393	2	US-08-621-751A-9
23	249.8	75.7	393	3	US-08-484-537-66
24	246.2	74.6	717	2	US-08-553-497A-17
25	245	74.2	906	2	US-08-656-906-24
26	245	74.2	906	3	US-09-217-847-24
27	243.4	73.8	333	1	US-08-442-542-3

28 243.4 73.8 333 3 US-08-765-469-3  
29 243.4 73.8 333 1 US-08-137-117D-24  
30 243.4 73.8 333 1 US-08-436-717-24  
31 243.4 73.8 1797 1 US-08-442-542-17  
32 243.4 73.8 1797 3 US-08-765-469-17  
33 242.4 73.5 783 4 US-08-487-283A-19  
34 239.4 72.5 333 1 US-08-207-169A-3  
35 238.6 72.3 336 3 US-09-065-059-14  
36 237 71.8 394 3 US-08-836-561-24  
37 237 71.8 394 4 US-09-434-122-24  
38 235.4 71.3 399 5 PCT-US94-14106-52  
39 235.4 71.3 428 3 US-08-589-939-4  
40 233.8 70.8 334 2 US-08-650-262-1  
41 233.8 70.8 723 5 PCT-US94-14106-56  
42 232.2 70.4 654 5 PCT-US96-13152-1  
43 231.4 70.1 332 3 US-08-881-037-58  
44 230.6 69.9 393 3 US-08-579-378A-17  
45 229 69.4 396 2 US-08-379-057-15

## ALIGNMENTS

RESULT 1  
US-08-483-636-1  
; Sequence 1, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMEJTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA: US 08/117366  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 396 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown







Best Local Similarity 88.9%; Pred. No. 2.9e-80;  
Matches 296; Conservative 0; Mismatches 34; Indels 3; Gaps 1;  
QY 1 GACATTGTCTCACCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
Db 61 GACATTGTCTCACCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 120  
QY 61 ATCTCTCGAAGCCAGCCAGCAAGTGTGATTATGATGTGATAGTATATG---TGGTAC 117  
Db 121 ATATCTCGAGAGCCAGTGAAGAGTGTGATAGTATGGAATAGTATGCACTGGTAC 180  
QY 118 CAACAGAACCCAGGACAGCCAGCCAACTCCTCAGCTATGCTGCAATCCAACTAGAAATCT 177  
Db 181 CAGCAGAACCCAGGACAGCCAGCCAACTCCTCAGCTATGCTGCAATCCAACTAGAAATCT 240  
QY 178 GGGATCCCAGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237  
Db 241 GGGATCCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 300  
QY 238 CTGTGGAGGAGGAGTCTGCAACCTATTAATCTGCTAGCTTTGTAATGAGATCCTGCC 297  
Db 301 CTGTGGAGGAGTGTGATGTTTCAACCTATTACTGTGCAAAAGTAAATGAGGATCCTGCC 360  
QY 298 AGCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330  
Db 361 AGCTTCGGTCTGGGACCAAGCTGGAGCTGAAA 393

RESULT 7  
US-08-275-053-10  
; Sequence 10, Application US/08275053  
; Patent No. 5607847  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Recombinant human anti-human immunodeficiency  
; virus antibody.  
; NUMBER OF SEQUENCES: 16  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/275,053  
; PRIOR APPLICATION NUMBER: PCT/GB93/01798  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 333 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
US-08-275-053-10

Query Match 79.1%; Score 261; DB 1; Length 333;  
Best Local Similarity 88.6%; Pred. No. 9.4e-80;  
Matches 295; Conservative 0; Mismatches 35; Indels 3; Gaps 1;  
QY 1 GACATTGTCTCACCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
Db 1 GACATTGTCTCACCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
QY 61 ATCTCTCGAAGCCAGCCAGCAAGTGTGATTATGATGTGATAGTATATG---TGGTAC 117  
Db 61 ATATCTCGAGAGCCAGTGAAGAGTGTGATAGTATGGAATAGTATGCACTGGTAC 120  
QY 118 CAACAGAACCCAGGACAGCCAGCCAACTCCTCAGCTATGCTGCAATCCAACTAGAAATCT 177  
Db 121 CAGCAGAACCCAGGACAGTCAACCACTCCTCAGCTATGCTGCAATCCAACTAGAAATCT 180  
QY 178 GGGATCCCAGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237

Db 181 GGGGTCCCTCCAGGTTCACTGGCAGTGGGTCTAGGACAGACTTCACCCCTCACCATTGAT 240  
QY 238 CCTGTGGAGAGAGAGATGCTGCAACTATTACTGTCTAGCTTTGTAATGAGGATCCTCCC 297  
Db 241 CCTGTGGAGGCTGATGCTGCAACCTATTACTGTGCAAAAATAATGAGGATCCGCTC 300  
QY 298 ACCTTCGGTCTCTGGGACCAAGCTGGAGCTGAAA 330  
Db 301 ACCTTCGGTCTCTGGGACCAAGCTGGAGCTGAAA 333

RESULT 8  
US-08-275-053-16/c  
; Sequence 16, Application US/08275053  
; Patent No. 5607847  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Recombinant human anti-human immunodeficiency  
; virus antibody.  
; NUMBER OF SEQUENCES: 16  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/275,053  
; PRIOR APPLICATION NUMBER: PCT/GB93/01798  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 333 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
US-08-275-053-16

Query Match 79.1%; Score 261; DB 1; Length 333;  
Best Local Similarity 88.6%; Pred. No. 9.4e-80;  
Matches 295; Conservative 0; Mismatches 35; Indels 3; Gaps 1;  
QY 1 GACATTGTCTCACCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
Db 333 GACATTGTCTCACCAGTCTCCAGCTTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 274  
QY 61 ATCTCTCGAAGCCAGCCAGCAAGTGTGATTATGATGTGATAGTATATG---TGGTAC 117  
Db 273 ATATCTCGAGAGCCAGTGAAGAGTGTGATAGTATGGAATAGTATGCACTGGTAC 214  
QY 118 CAACAGAACCCAGGACAGCCAGCCAACTCCTCAGCTATGCTGCAATCCAACTAGAAATCT 177  
Db 213 CAGCAGAACCCAGGACAGTCAACCACTCCTCAGCTATGCTGCAATCCAACTAGAAATCT 154  
QY 178 GGGATCCCAGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237  
Db 153 GGGGTCCCTCCAGGTTCACTGGCAGTGGGTCTAGGACAGACTTCACCCCTCACCATTGAT 94  
QY 238 CCTGTGGAGAGAGAGTCTGCAACCTATTACTGTGAGCTTTGTAATGAGGATCCTCCC 297  
Db 93 CCTGTGGAGGCTGATGCTGCAACCTATTACTGTGCAAAAATAATGAGGATCCGCTC 34  
QY 298 ACCTTCGGTCTCTGGGACCAAGCTGGAGCTGAAA 330  
Db 33 ACCTTCGGTCTCTGGGACCAAGCTGGAGCTGAAA 1

RESULT 9  
US-08-111-080-21  
; Sequence 21, Application 08/111080  
; Patent No. 5558865  
; GENERAL INFORMATION:  
; APPLICANT: Ohno, Tsuneya



	Query Match	79.1%	Score 261;	DB 1;	Length 363;
	Best Local Similarity	88.6%	Pred. No. 9.8e-80;		
	Matches 295;	Conservative	0;	Mismatches 35;	Indels 3; Gaps 1;
QY	1	GACATTGTGCTCACCAATTC	TCCAGCTCTCTTTGGCTGTGTCT	TAGGGCAGAGGGCCACC	60
Db	1	GACATTGTGCTGACCAATCT	CCCAGCTCTCTTTGGCTGTGTCT	TAGGGCAGAGGGCCACC	60
QY	61	ATCTCTGCAAGCCAGCCAAAGTGTG	TATATATGATGGTGATAGTTATATG	---TGTGAC	117
Db	61	ATATCTGCAAGCCAGTGAAAGTGTG	TATATGATGGCAATAGTTTATGCACTG	GATAC	120
QY	118	CAACAGAAACCGAGCAGCCACC	CCAACTCTCACTATGCTGCATCC	CAATCTAGAAATCT	177
Db	121	CAGCAGAAACCGAGCAGTCA	CCCAACTCTCATATGTTGCATCC	ACCTAGAAATCT	180
QY	178	GGGATCCCAGCCAGGTTTATG	TGGCAGTGGGTCTGGGACAGACT	TTCACCTTCACATCCAT	237

Db 181 GGGTCCCTCCGAGGTTCAAGTGGCAGTGGTCTAGGACAGACTTCACCTCCACCAATTGAT 240  
QY 238 CTTGTGGAGGAGGAGGATGCTCAACCTATTACTGTCAAGCTTTGTAATGAGGATCCTCCC 297  
Db 241 CTTGTGGAGGCTGATGATGCTCAACCTATTACTGTCAAGCAAAATTAATGAGGATCCGCTC 300  
QY 298 AGTTTCGGTGTGGGACCAAGCTGGAGCTGAAA 330  
Db 301 ACCTTCGGTGTGGGACCAAGCTGGAGCTGAAA 333

## RESULT 11

PCT-US93-07967-21  
; Sequence 21, Application PC/TUS9307967  
; GENERAL INFORMATION:  
; APPLICANT: Ohno, Tsuneya  
; TITLE OF INVENTION: HIV Immunotherapeutics  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSER: Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07967  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07111  
; FILING DATE: 24-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/039,457  
; FILING DATE: 22-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 31629  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 363 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..363

## PCT-US93-07967-21

Query Match 79.1%; Score 261; DB 5; Length 363;  
Best Local Similarity 88.6%; Pred. No. 9.8e-80;  
Matches 295; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCATTCTCCAGTCTTTTGGCTGTCTCTAGGCGAGAGGCGCCACC 60  
Db 1 GACATTGTGCTGACCCATCTCCAGTCTTTTGGCTGTCTCTAGGCGAGAGGCGCCACC 60  
QY 61 ATCTCCTGCAAGGCGAGCCCAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 117  
Db 61 ATATCTGCGAGAGGCGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 120

QY 118 CAACAGAAACAGGACAGCCACCAACTCTCACCTATGTGTCATCCCAATCTAGAACTCT 177  
Db 121 CAGCAGAAACAGGACAGTCAACCAACTCTCTATGTTGTCATCCCACTAGAACTCT 180  
QY 178 GGGATCCAGCCAGGTTTATGTGTCATGTTGGGACAGACTTCCACCTCAACATCCAT 237  
Db 181 GGGGTCCCTGCCAGGTTTCAAGTGGCAGTGGTCTAGGACAGACTTCCACCTCAACATGAT 240  
QY 238 CTTGTGGAGGAGGAGGATGCTCAACCTATTACTGTCAAGCTTTGTAATGAGGATCCTCCC 297  
Db 241 CTTGTGGAGGCTGATGATGCTCAACCTATTACTGTCAAGCAAAATTAATGAGGATCCGCTC 300  
QY 298 ACCTTCGGTGTGGGACCAAGCTGGAGCTGAAA 330  
Db 301 ACCTTCGGTGTGGGACCAAGCTGGAGCTGAAA 333

## RESULT 12

US-08-553-497A-9  
; Sequence 9, Application US/08553497A  
; Patent No. 5844093  
; GENERAL INFORMATION:  
; APPLICANT: KETTLERBROUGH, C. A.  
; APPLICANT: BENDIG, MARY M.  
; APPLICANT: ANSELL, KEITH H.  
; APPLICANT: GUSSOW, DETLEF  
; APPLICANT: ADAN, JAUME  
; APPLICANT: MITTANS, FRANCES  
; APPLICANT: ROSELL, ELISABET  
; APPLICANT: BLASCO, FRANCES  
; APPLICANT: PIULATS, JAUME  
; TITLE OF INVENTION: ANTI-BGFR SINGLE-CHAIN FVS AND ANTI-BGFR  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
; STREET: 2200 CLARENDON BLVD. SUITE 1400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,497A  
; FILING DATE: 17-NOV-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/00978  
; FILING DATE: 16-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94104160.0  
; FILING DATE: 17-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94118970.6  
; FILING DATE: 02-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HAWLET-KING, DIANA  
; REGISTRATION NUMBER: 33,302  
; REFERENCE/DOCKET NUMBER: MERCK 1726  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-243-6333  
; TELEFAX: 703-243-6410  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 339 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA

```
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: mouse
; STRAIN: Balb/c
; DEVELOPMENTAL STAGE: adult
; TISSUE TYPE: Lymph node
; IMMEDIATE SOURCE:
; CLONE: L3 11D (light chain)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; US-08-553-497A-9

Query Match      78.1%; Score 257.8; DB 2; Length 339;
Best Local Similarity 88.0%; Pred. No. 1.2e-78;
Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCAGTTCACAGCTTCTTTGGCTGTGTCTTAGGGCAGAGGCCACC 60
DB 1 GACATTGAGCTCACCAGTTCACAGCTTCTTTGGCTGTGTCTTAGGGCAGAGGCCACC 60
QY 61 ATCTCTCAAGCCAGCCAGCAAGTGTGATTATGATGTGATAGTATATG---TGGTAC 117
DB 61 ATCTCTGCCAGCCAGCCAGCAAGTGTGATTATGATGTGATAGTATATG---TGGTAC 120
QY 118 CAACAGAAACCCAGGACGCCACCAAACTCTCTACCTATGTCTGATCCATCCATCTAGAAATCT 177
DB 121 CAACAGAAACCCAGGACGCCACCAAACTCTCTACCTATGTCTGATCCATCCATCCATCTAGAAATCT 180
QY 178 GGGATCCAGCCAGCTTTAGTGGCAGTGGGCTGGGACAGACTTCCCTCAACATCCAT 237
DB 181 GGGATCCAGCTTTAGTGGCAGTGGGCTGGGACAGACTTCCCTCAACATCCAT 240
QY 238 CTTGTGGAGGAGGAGTGTGCAACCTATTACTGTGAGCTTTTGTATAGGAGTCTCC 297
DB 241 CTTGTGGAGGAGGAGTGTGCAACCTATTACTGTGAGCTTTTGTATAGGAGTCTCC 300
QY 298 ACGTTTCGGTGTGGACCAAGCTGGAGCTGAAA 330
DB 301 ACGTTTCGGTGTGGACCAAGCTGGAGCTGAAA 333

RESULT 13
US-08-111-080-17
; Sequence 17, Application 08/11/080
; Patent No. 555865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..363
; US-08-111-080-17

Query Match      78.1%; Score 257.8; DB 1; Length 363;
Best Local Similarity 88.0%; Pred. No. 1.2e-78;
Matches 293; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 1 GACATTGTGCTCACCAGTTCACAGCTTCTTTGGCTGTGTCTTAGGGCAGAGGCCACC 60
DB 1 GACATTGTGCTCACCAGTTCACAGCTTCTTTGGCTGTGTCTTAGGGCAGAGGCCACC 60
QY 61 ATCTCTCAAGCCAGCCAGCAAGTGTGATTATGATGTGATAGTATATG---TGGTAC 117
DB 61 ATCTCTGCCAGCCAGCCAGCAAGTGTGATTATGATGTGATAGTATATG---TGGTAC 120
QY 118 CAACAGAAACCCAGGACGCCACCAAACTCTCTACCTATGTCTGATCCATCCATCTAGAAATCT 177
DB 121 CAACAGAAACCCAGGACGCCACCAAACTCTCTACCTATGTCTGATCCATCCATCTAGAAATCT 180
QY 178 GGGATCCAGCCAGCTTTAGTGGCAGTGGGCTGGGACAGACTTCCCTCAACATCCAT 237
DB 181 GGGATCCAGCTTTAGTGGCAGTGGGCTGGGACAGACTTCCCTCAACATCCAT 240
QY 238 CTTGTGGAGGAGGAGTGTGCAACCTATTACTGTGAGCTTTTGTATAGGAGTCTCC 297
DB 241 CTTGTGGAGGAGGAGTGTGCAACCTATTACTGTGAGCTTTTGTATAGGAGTCTCC 300
QY 298 ACGTTTCGGTGTGGACCAAGCTGGAGCTGAAA 330
DB 301 ACGTTTCGGTGTGGACCAAGCTGGAGCTGAAA 333

RESULT 14
US-08-211-980-17
; Sequence 17, Application US/08211980
; Patent No. 5665569
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

RESULT 15  
PCT-US92-07111-16  
; Sequence 16, Application PC/TUS9207111  
; GENERAL INFORMATION:  
; APPLICANT: Ohno, Tsuneya  
; TITLE OF INVENTION: HIV Immunotherapeutics  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street

Search completed: January 14, 2004, 17:48:18  
Job time : 42 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2004, 16:03:20 ; Search time 196.19 Seconds  
(without alignments)  
5928.789 Million cell updates/sec

```

Title: US-09-759-112A-22
Perfect score: 330
Sequence: 1 gacattgtgtccacaattc.....ggaccaagctggagctgaaa 330

```

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 176238165

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:1

```

Database :
Published_applications_NA:
1: /cgn2/6/prodata1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2/6/prodata1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2/6/prodata1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2/6/prodata1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2/6/prodata1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2/6/prodata1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2/6/prodata1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2/6/prodata1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2/6/prodata1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2/6/prodata1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2/6/prodata1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2/6/prodata1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2/6/prodata1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2/6/prodata1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2/6/prodata1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2/6/prodata1/pubpna/US10_NEW_PUB.seq.*
17: /cgn2/6/prodata1/pubpna/US60_NEW_PUB.seq.*
18: /cgn2/6/prodata1/pubpna/US60_PUBCOMB.seq.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	330	100.0		330	11	US-09-759-112A-22	Sequence 22, Appl
2	330	100.0		330	11	US-09-759-112A-23	Sequence 23, Appl
3	294.6	89.3		396	10	US-09-879-461-1	Sequence 1, Appl
4	293	88.8		714	13	US-10-384-933-10	Sequence 10, Appl
5	293	88.8		714	15	US-10-216-484-10	Sequence 10, Appl
6	286.6	86.8		831	10	US-09-932-327A-3	Sequence 3, Appl
7	275.4	83.5		768	13	US-10-384-933-53	Sequence 53, Appl
8	275.4	83.5		768	15	US-10-216-484-53	Sequence 53, Appl
9	272.2	82.5		768	13	US-10-384-933-51	Sequence 51, Appl
10	272.2	82.5		768	13	US-10-384-933-108	Sequence 108, Appl
11	272.2	82.5		768	15	US-10-216-484-51	Sequence 51, Appl
12	272.2	82.5		768	15	US-10-216-484-108	Sequence 108, Appl
13	272.2	82.5		825	13	US-10-053-530-8	Sequence 8, Appl
14	272.2	82.5		825	15	US-10-207-655-8	Sequence 8, Appl
15	262.6	79.6		393	9	US-09-286-240-1	Sequence 1, Appl

16	256.2	77.6	768	13	US-10-384-933-106	Sequence 106, App
17	256.2	77.2	768	13	US-10-216-484-106	Sequence 106, App
18	254.6	77.2	768	13	US-10-384-933-49	Sequence 49, Appl
19	254.6	77.2	768	13	US-10-216-484-49	Sequence 49, Appl
20	253	76.7	717	13	US-10-353-708-37	Sequence 37, Appl
21	253	76.7	717	13	US-10-353-708-43	Sequence 43, Appl
22	253	76.7	717	13	US-10-353-708-49	Sequence 49, Appl
23	253	76.7	717	13	US-10-353-708-55	Sequence 55, Appl
24	253	76.7	717	15	US-10-171-452A-37	Sequence 37, Appl
25	253	76.7	717	15	US-10-171-452A-43	Sequence 43, Appl
26	253	76.7	717	15	US-10-171-452A-49	Sequence 49, Appl
27	253	76.7	717	15	US-10-171-452A-55	Sequence 55, Appl
28	249.8	75.7	393	12	US-10-389-155-57	Sequence 57, Appl
29	246.6	74.7	420	9	US-09-881-823-1	Sequence 1, Appl
30	245	74.2	336	13	US-10-169-351-67	Sequence 67, Appl
31	245	74.2	351	13	US-10-169-351-68	Sequence 68, Appl
32	244	73.9	438	12	US-09-791-551-53	Sequence 53, Appl
33	243.4	73.8	405	15	US-10-207-655-249	Sequence 249, App
34	243.4	73.8	828	15	US-10-207-655-253	Sequence 253, App
35	243.4	73.8	1683	15	US-10-207-655-267	Sequence 267, App
36	241.8	73.3	809	14	US-10-027-770-1	Sequence 1, Appl
37	238.6	72.3	333	13	US-10-160-508-76	Sequence 76, Appl
38	238.6	72.3	333	13	US-10-160-508-78	Sequence 78, Appl
39	237.6	72.0	780	13	US-10-244-821-46	Sequence 46, Appl
40	237.6	72.0	780	15	US-10-013-173-46	Sequence 46, Appl
41	237.6	72.0	780	15	US-10-150-763-46	Sequence 46, Appl
42	237	71.8	394	15	US-10-283-349-24	Sequence 24, Appl
43	232.8	70.5	783	13	US-10-244-821-36	Sequence 36, Appl
44	232.8	70.5	783	15	US-10-013-173-36	Sequence 36, Appl
45	232.8	70.5	783	15	US-10-150-763-36	Sequence 36, Appl

## ALIGNMENTS

```

RESULT 1
US-09-759-112A-22
/ Sequence 22, Application US/09759112A
/ Publication No. US20030100741A1
/ GENERAL INFORMATION:
/ APPLICANT: Mueller, Sybille
/ APPLICANT: Kohler, Heinz
/ TITLE OF INVENTION: NUCLEOTIDE SEQUENCES
/ TITLE OF INVENTION: OF MONOCLONAL ANTIBODIES
/ TITLE OF INVENTION: ANTIBODIES
/ FILE REFERENCE: 200-013
/ CURRENT APPLICATION NUMBER: US/09/759-112A-22
/ CURRENT FILING DATE: 2001-01-11
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 22
/ LENGTH: 330
/ TYPE: DNA
/ ORGANISM: mouse
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1)..(330)
/ OTHER INFORMATION: 1F7 VL chain gene
US-09-759-112A-22

```

	Query Match	100.0%;	Score 330;	DB 11;	Length 330;
	Best Local Similarity	100.0%;	Pred. No. 8.1e-104;		
	Matches 330;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GACATTGTGCTACCAATTCTCCAGCTTCTTTGGCTGTGTCCTTAGGGCAGAGGCCACC	60		
Db	1	GACATTGTGCTACCAATTCTCCAGCTTCTTTGGCTGTGTCCTTAGGGCAGAGGCCACC	60		
QY	61	ATCTCCTGCAAGCCAGCCAGCAAGTGTGATTATGATGGTATAGTATATGTGTACCA	120		
Db	61	ATCTCTGCAAGCCAGCCAGCAAGTGTGATTATGATGGTATAGTATATGTGTACCA	120		
QY	121	CAGAAACAGGACAGCCAGCCACCAACTCTTCACCTATGCTGCATCCAACTAGAACTCTGGG	180		



QY 298 ACGTTCGGTGTCTGGGACCAAGCTGGAGCTGAAA 330  
|||||  
Db 361 ACGTTCGGTGGAGGCCAAGCTGGAAATCAAA 393

## RESULT 4

US-10-384-933-10  
; Sequence 10, Application US/10384933  
; Publication No. US20030170817A1  
; GENERAL INFORMATION:  
; APPLICANT: Serizawa, NO. US20030170817A1ufusa  
; APPLICANT: Haryuyama, Hideyuki  
; APPLICANT: Nakahata, Kaori  
; APPLICANT: Tamaki, Ikuko  
; APPLICANT: Takahashi, Tohru  
; TITLE OF INVENTION: Anti-Pas Antibodies  
; FILE REFERENCE: 980126CIP/HG  
; CURRENT APPLICATION NUMBER: US/10/384,933  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US/09/499,662  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01  
; NUMBER OF SEQ ID NOS: 165

Query Match 88.8%; Score 293; DB 13; Length 714;  
Best Local Similarity 94.6%; Pred. No. 7.3e-91;  
Matches 315; Conservative 0; Mismatches 15; Indels

RESULT 5  
US-10-216-484-10  
; Sequence 10, Application US/10216484  
; Publication No. US20030103976A1

## RESULT 5

US-10-216-484-10  
; Sequence 10, Application US/10216484  
; Publication No. US20030103976A1

```

: GENERAL INFORMATION:
: APPLICANT: Saruzawa, No. US20030103976A1ufusa
: APPLICANT: Harizawa, Hideyuki
: APPLICANT: Nakahara, Kaori
: APPLICANT: Tamaki, Tsuko
: APPLICANT: Takahashi, Tohru
: TITLE OF INVENTION: Anti-Fas Antibodies
: FILE REFERENCE: 980126CIP/HG
: CURRENT APPLICATION NUMBER: US/10/216,484
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: US/09/499,662
: PRIOR FILING DATE: 2000-02-09
: PRIOR APPLICATION NUMBER: US 09/053,583
: PRIOR FILING DATE: 1998-04-01
: NUMBER OF SEQ IDS:165

```

Query Match	88.8%; Score 293; DB 15; Length 714;
Best Local Similarity	94.6%; Pred. No. 7.3e-91;
Matches 315; Conservative 0; Mismatches 15; Indels 3; Gaps 1;	
Qy	1 GCAATTGTCACCAATCTCCAGCTTCTTTGGCTGTGTCCTTAGGGCAGAGGGCCACC 60
Db	120
Qy	61 GCAATTGTGTGACCCAAATCTCCAGCTTCTTTGGCTGTGTCCTTAGGGCAGAGGGCCACC 120
Db	117
Qy	121 ATCTCTGCAAGCCAGCCAAAGTGTGTGATTATGATGGTGATAGTTATATG---TGGTAC 117
Db	180
Qy	118 CAAACAGAAACGAGGACAGGCCACCCAAACTCTTCACTATGCTGCATCCCAATCTAGAAATCT 177
Db	177
Qy	181 CAAACAGAAACGAGGACAGGCCACCCAAACTCTTCACTATGCTGCATCCCAATCTAGAAATCT 240
Db	240
Qy	178 GGGATCCCAGCCAGGTTTATGTGCACTGGGTCTGGACACAGACTTTCACCCCTCAACATCCAT 237
Db	237
Qy	241 GGGATCCCAGCCAGGTTTATGTGCACTGGGTCTGGACACAGACTTTCACCCCTCAACATCCAT 300
Db	300
Qy	238 CTTGTGGAGGAGGAGGATGCTGCAACTATTACTGTCAAGTTTGTAAATGAGGATCCTCCC 297
Db	297
Qy	301 CTTGTGGAGGAGGAGATGCTGCAACTTATTACTGTCAACAAAGTAATGAGGATCCTCGG 360
Db	360
Qy	298 AGCTTCGGTGTGGGACCAAGCTGGAGCTGAAA 330
Db	330
Qy	361 AGCTTCGGTGGAGGACCAAGCTGGAAATCAA 393
Db	393

RESULT 6  
US-09-903-327A-3  
; Sequence 3, Application US/09903327A  
; Patent No. US20020164333A1  
; GENERAL INFORMATION:  
; APPLICANT: Nemetow, Glen R.  
; APPLICANT: Li, Erguang  
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND V  
; TITLE OF INVENTION: GENE  
; TITLE OF INVENTION: DELIVERY  
; FILE REFERENCE: 22908-1228  
; CURRENT APPLICATION NUMBER: US/09/903,327A  
; CURRENT FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: 09/613,017

```

; LOCATION: (40)...(99)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
; OTHER INFORMATION: encoding the light chain of humanized anti-human
; OTHER INFORMATION: Fas antibody
US-10-384-933-53

Query Match      83.5%; Score 275.4; DB 13; Length 768;
Best Local Similarity 91.3%; Pred. No. 9.5e-85;
Matches 304; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 1 GACATTGTGCTACCAAAATCTCCAGCTCTCTTGGCTGCTCTCTAGGGCAGAGGGCCACC 60
Db 100 GACATTGTGCTACCAAAATCTCCAGTACTTTGTCTCTCTCCAGGGAGAGGGCCACC 159
QY 61 ATCTCTGCAAGCCAGCCAGCAAAAGTGTGTGATATGATGGTGAAGTTATATG---TGGTAC 117
Db 160 CTCTCTGCAAGCCAGCCAGCAAAAGTGTGTGATATGATGGTGAAGTTATATGAATCGGTAC 219
QY 118 CACAGAAACCCAGGACAGCCACCCAAACTCTCCACCTATGCTGCATCCCAATCTAGAAATCT 177
Db 220 CACAGAAACCCAGGACAGCCACCCAAACTCTCATCTATGCTGCATCCCAATCTCGAATCT 279
QY 178 GGGATCCCAAGCCAGGTTTATGTGSCAGTGGGTCTGGGACACAGACTTCACCCCTCAACATCCAT 237
Db 280 GGGATCCCAAGACAGGTTTATGTGSCAGTGGGTCTGGGACACAGACTTCACCCCTCAACATCCAT 339
QY 238 CCTGTGGAGGAGGAGATGCTGCAACTTATTACTGTCACTTTGTGAATGAGGATCTCTCCC 297
Db 340 CCTGTGGAGGAGGAGATGCTGCAACTTATTACTGTCAAGAAAGTAATGAGGATCTCTCG 399
QY 298 ACGTTCGGTGCCTGGGACCAAGCTGGAGCTGAAA 330
Db 400 ACGTTCGGTCAAGGCACACAGGCTGGAAATCAAA 432

RESULT 8
US-10-216-484-53
; Sequence 53, Application US/10216484
; Publication No. US20030103976A1

```

```

/ APPLICANT: Srizawa, No. US20030103976A1ufusa
/
/ APPLICANT: Haruyama, Hideyuki
/
/ APPLICANT: Nakahara, Kaori
/
/ APPLICANT: Tamaki, Ikuko
/
/ APPLICANT: Takahashi, Tohru
/
/ TITLE OF INVENTION: Anti-Fas Antibodies
/
/ FILE REFERENCE: 980126CIP/HG
/
/ CURRENT APPLICATION NUMBER: US/10/216,484
/
/ CURRENT FILING DATE: 2002-08-09
/
/ PRIOR APPLICATION NUMBER: US/09/499,662
/
/ PRIOR FILING DATE: 2000-02-09
/
/ PRIOR APPLICATION NUMBER: US 09/053,583
/
/ PRIOR FILING DATE: 1998-04-01
/
/ NUMBER OF SEQ ID NOS: 165
/
/ SEQ ID NO 53
/
/ LENGTH: 768
/
/ TYPE: DNA
/
/ ORGANISM: Artificial Sequence
/
/ FEATURE:
/
/ NAME/KEY: CDS
/
/ LOCATION: (40)..(753)
/
/ FEATURE:
/
/ NAME/KEY: mat peptide
/
/ LOCATION: (100)..(753)
/
/ FEATURE:
/
/ NAME/KEY: sig peptide
/
/ LOCATION: (40)..(99)
/
/ FEATURE:
/
/ OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
/
/ OTHER INFORMATION: encoding the light chain of humanized anti-human
/
/ OTHER INFORMATION: Fas antibody
/
/ US-10-216-484-53

```



Query Match 83.5%; Score 275.4; DB 15; Length 768;  
Best Local Similarity 91.3%; Pred. No. 9.5e-85;  
Matches 304; Conservative 0; Mismatches 26; Indels 3; Gaps 1;  
QY 1 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
DB 100 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 159  
QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTGATGGTGATAGTTATATG---TGGTAC 117  
DB 160 CTCTCTGCAAGCCAGCCAAAGTGTGATTGATGGTGATAGTTATATG---TGGTAC 219  
QY 118 CAACAGAAACCCAGGACAGCCACCAACTCTCTACCTATCTGTCATCTATGTCGATCTCAATCTGAAATCT 177  
DB 220 CAACAGAAACCCAGGACAGCCACCAACTCTCTACCTATCTGTCATCTATGTCGATCTCAATCTGAAATCT 219  
QY 178 GGGATCCAGCCAGGTTTGTAGTGGCAGTCTGGGACAGACTTCCACCTCAACATCCAT 237  
DB 280 GGGATCCAGGACAGCTTTAGTGGCAGTCTGGGACAGACTTCCACCTCAACATCCAT 339  
QY 238 CCTGTGGAGGAGGAGTCTGCAACTATTATCTGTCAGCTTTGTAATGAGGATCTCTCC 297  
DB 340 CCTGTGGAGGAGGAGTCTGCAACTATTATCTGTCAGCTTTGTAATGAGGATCTCTCG 399  
QY 298 ACGTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330  
DB 400 ACGTTCGGTCAAGGACCAAGCTGGAGCTGAAA 432

RESULT 9  
US-10-384-933-51  
; Sequence 51, Application US/10384933  
; Publication No. US20030170817A1  
; GENERAL INFORMATION:  
; APPLICANT: Serizawa, No. US20030170817A1ufusa  
; APPLICANT: Haruyama, Hideyuki  
; APPLICANT: Nakahara, Kaori  
; APPLICANT: Tamaki, Ikuko  
; APPLICANT: Takahashi, Tohru  
; TITLE OF INVENTION: Anti-Fas Antibodies  
; FILE REFERENCE: 980126CIP/HG  
; CURRENT APPLICATION NUMBER: US/10/384,933  
; PRIOR FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US/09/499,662  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 51  
; LENGTH: 768  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (40)..(753)  
; FEATURE:  
; NAME/KEY: mat peptide  
; LOCATION: (100)..(753)  
; FEATURE:  
; NAME/KEY: sig peptide  
; LOCATION: (40)..(99)  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA  
; OTHER INFORMATION: encoding the light chain of humanized anti-human  
; OTHER INFORMATION: Fas antibody  
US-10-384-933-51  
Query Match 82.5%; Score 272.2; DB 13; Length 768;  
Best Local Similarity 90.7%; Pred. No. 1.2e-83;  
Matches 302; Conservative 0; Mismatches 28; Indels 3; Gaps 1;  
QY 1 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60

DB 100 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 159  
QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTGATGGTGATAGTTATATG---TGGTAC 117  
DB 160 CTCTCTGCAAGCCAGCCAAAGTGTGATTGATGGTGATAGTTATATG---TGGTAC 219

DB 100 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 159  
QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTGATGGTGATAGTTATATG---TGGTAC 117  
DB 160 CTCTCTGCAAGCCAGCCAAAGTGTGATTGATGGTGATAGTTATATG---TGGTAC 219  
QY 118 CAACAGAAACCCAGGACAGCCACCAACTCTCTACCTATCTGTCATCTATGTCGATCTCAATCTGAAATCT 177  
DB 220 CAACAGAAACCCAGGACAGCCACCAACTCTCTACCTATCTGTCATCTATGTCGATCTCAATCTGAAATCT 219  
QY 178 GGGATCCAGCCAGGTTTGTAGTGGCAGTCTGGGACAGACTTCCACCTCAACATCCAT 237  
DB 280 GGGATCCAGGACAGCTTTAGTGGCAGTCTGGGACAGACTTCCACCTCAACATCCAT 339  
QY 238 CCTGTGGAGGAGGAGTCTGCAACTATTATCTGTCAGCTTTGTAATGAGGATCTCTCC 297  
DB 340 CCTGTGGAGGAGGAGTCTGCAACTATTATCTGTCAGCTTTGTAATGAGGATCTCTCG 399  
QY 298 ACGTTCGGTCTGGGACCAAGCTGGAGCTGAAA 330  
DB 400 ACGTTCGGTCAAGGACCAAGCTGGAGCTGAAA 432

RESULT 10  
US-10-384-933-108  
; Sequence 108, Application US/10384933  
; Publication No. US20030170817A1  
; GENERAL INFORMATION:  
; APPLICANT: Serizawa, No. US20030170817A1ufusa  
; APPLICANT: Haruyama, Hideyuki  
; APPLICANT: Nakahara, Kaori  
; APPLICANT: Tamaki, Ikuko  
; APPLICANT: Takahashi, Tohru  
; TITLE OF INVENTION: Anti-Fas Antibodies  
; FILE REFERENCE: 980126CIP/HG  
; CURRENT APPLICATION NUMBER: US/10/384,933  
; PRIOR FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US/09/499,662  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 108  
; LENGTH: 768  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (40)..(753)  
; FEATURE:  
; NAME/KEY: mat peptide  
; LOCATION: (100)..(753)  
; FEATURE:  
; NAME/KEY: sig peptide  
; LOCATION: (40)..(99)  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA  
; OTHER INFORMATION: encoding the light chain of a humanized anti-Fas  
; OTHER INFORMATION: antibody  
US-10-384-933-108  
Query Match 82.5%; Score 272.2; DB 13; Length 768;  
Best Local Similarity 90.7%; Pred. No. 1.2e-83;  
Matches 302; Conservative 0; Mismatches 28; Indels 3; Gaps 1;  
QY 1 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 60  
DB 100 GACATTGTGCTCACCACCAATCTCCAGCTCTTTGGCTGTCTCTAGGGCAGAGGCCACC 159  
QY 61 ATCTCTGCAAGCCAGCCAAAGTGTGATTGATGGTGATAGTTATATG---TGGTAC 117  
DB 160 CTCTCTGCAAGCCAGCCAAAGTGTGATTGATGGTGATAGTTATATG---TGGTAC 219

QY 118 CAACAGAAACAGGACAGCCACCCAAACTCCTACCTATGCTGCATCCAAATCTAGAAATCT 177  
Db 220 CAACAGAAACAGGACAGCCACCCAGACTCTCTCATCTATGCTGCATCCAAATCTGAAATCT 279  
QY 178 GGGATCCAGACAGGTTTAGTGAGGAGTGGTCTGGGACAGACTTCAGCCTCAACATCCAT 237  
Db 280 GGGATCCAGACAGGTTTAGTGAGGAGTGGTCTGGGACAGACTTCAGCCTCAACATCCAT 339  
QY 238 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTGAGCTTTGTAATGAGGATCCTCC 297  
Db 340 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTGAGCTTTGTAATGAGGATCCTCGG 399  
QY 298 ACGTTCGGTGTGGACCAAGCTGAGCTGAAA 330  
Db 400 ACGTTCGGTCAAGGACCAAGCTGGAATCAAA 432

## RESULT 11

US-10-216-484-51  
; Sequence 51, Application US/10216484  
; Publication No. US20030103976A1  
; GENERAL INFORMATION:  
; APPLICANT: Serizawa, No. US20030103976Alufusa  
; APPLICANT: Haruyama, Hideyuki  
; APPLICANT: Nakahara, Kaori  
; APPLICANT: Takaki, Ikuko  
; APPLICANT: Takahashi, Tohru  
; TITLE OF INVENTION: Anti-Fas Antibodies  
; FILE REFERENCE: 980126CIP/HG  
; CURRENT APPLICATION NUMBER: US/10/216.484  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US/09/499,662  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 09/053,583  
; PRIOR FILING DATE: 1998-04-01  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 51  
; LENGTH: 768  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (40)..(753)  
; NAME/KEY: mat peptide  
; LOCATION: (100)..(753)  
; FEATURE:  
; NAME/KEY: sig peptide  
; LOCATION: (40)..(99)  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA  
; OTHER INFORMATION: encoding the light chain of humanized anti-human  
; OTHER INFORMATION: Fas antibody  
US-10-216-484-51

Query Match 82.5%; Score 272.2; DB 15; Length 768;  
Best Local Similarity 90.7%; Pred. No. 1.2e-83;  
Matches 302; Conservative 0; Mismatches 28; Indels 3; Gaps 1;  
QY 1 GACATTGTGCTCACCATTCTCCAGCTTCTTGGCTGTGCTCTAGGGCAGAGGGCCACC 60  
Db 100 GACATTGTGCTCACCATTCTCCAGTACTTTGTCTCTGTCTCCAGGGAGAGGGCCACC 159  
QY 61 ATCTCTCTCAAGGCGCAGCAAGTGTGATTATGATGGTGTATAGTTATATG---TGGTAC 117  
Db 160 CTCTCTCTCAAGGCGCAGCAAGTGTGATTATGATGGTGTATATGAACTGTGTAC 219  
QY 118 CAACAGAAACAGGACAGCCACCAACTCTACCTATGCTGCATCCAAATCTAGAAATCT 177  
Db 220 CAACAGAAACAGGACAGCCACCCAGACTCTCTCATCTATGCTGCATCCAAATCTGAAATCT 279  
QY 178 GGGATCCAGGACAGGTTTAGTGAGGAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237

Db 280 GGGATCCAGACAGGTTTAGTGAGGAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 339  
QY 238 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTGAGCTTTGTAATGAGGATCCTCC 297  
Db 340 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTGAGCTTTGTAATGAGGATCCTCGG 399  
QY 298 ACGTTCGGTGTGGACCAAGCTGAGCTGAAA 330  
Db 400 ACGTTCGGTCAAGGACCAAGCTGGAATCAAA 432

## RESULT 12

US-10-216-484-108  
; Sequence 108, Application US/10216484  
; Publication No. US20030103976A1  
; GENERAL INFORMATION:  
; APPLICANT: Serizawa, No. US20030103976Alufusa  
; APPLICANT: Haruyama, Hideyuki  
; APPLICANT: Nakahara, Kaori  
; APPLICANT: Tamaki, Ikuko  
; APPLICANT: Takahashi, Tohru  
; TITLE OF INVENTION: Anti-Fas Antibodies  
; FILE REFERENCE: 980126CIP/HG  
; CURRENT APPLICATION NUMBER: US/10/216.484  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US/09/499,662  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 09/053,583  
; PRIOR FILING DATE: 1998-04-01  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 108  
; LENGTH: 768  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (40)..(753)  
; NAME/KEY: mat peptide  
; LOCATION: (100)..(753)  
; FEATURE:  
; NAME/KEY: sig peptide  
; LOCATION: (40)..(99)  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA  
; OTHER INFORMATION: encoding the light chain of a humanized anti-Fas  
; OTHER INFORMATION: antibody  
US-10-216-484-108

Query Match 82.5%; Score 272.2; DB 15; Length 768;  
Best Local Similarity 90.7%; Pred. No. 1.2e-83;  
Matches 302; Conservative 0; Mismatches 28; Indels 3; Gaps 1;  
QY 1 GACATTGTGCTCACCATTCTCCAGCTTCTTGGCTGTGCTCTAGGGCAGAGGGCCACC 60  
Db 100 GACATTGTGCTCACCATTCTCCAGTACTTTGTCTCTGTCTCCAGGGAGAGGGCCACC 159  
QY 61 ATCTCTCTCAAGGCGCAGCAAGTGTGATTATGATGGTGTATAGTTATATG---TGGTAC 117  
Db 160 CTCTCTCTCAAGGCGCAGCAAGTGTGATTATGATGGTGTATATGAACTGTGTAC 219  
QY 118 CAACAGAAACAGGACAGCCACCAACTCTACCTATGCTGCATCCAAATCTAGAAATCT 177  
Db 220 CAACAGAAACAGGACAGCCACCCAGACTCTCTCATCTATGCTGCATCCAAATCTGAAATCT 279  
QY 178 GGGATCCAGGACAGGTTTAGTGAGGAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 237  
Db 280 GGGATCCAGGACAGGTTTAGTGAGGAGTGGTCTGGGACAGACTTCACCCCTCAACATCCAT 339  
QY 238 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTGAGCTTTGTAATGAGGATCCTCC 297  
Db 340 CTTGTGGAGGAGGAGTCTGCAACCTATTACTGTGAGCTTTGTAATGAGGATCCTCGG 399





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 17:47:02 ; Search time 33.8095 Seconds  
(without alignments)  
516.420 Million cell updates/sec

Title: US-09-759-112A-24  
Perfect score: 582  
Sequence: 1 DIVTNSPASLAVSLGQRAT.....COLCNEPPTFGATKLELK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues 1107863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	100.0	110	23	AAO18536
2	537.5	92.4	132	16	AAO18536
3	537.5	92.4	132	20	AAO18536
4	537.5	92.4	132	20	AAO18536
5	532.5	91.5	111	21	AAO18536
6	532.5	91.5	111	21	AAO18536
7	532.5	91.5	111	21	AAO18536
8	532.5	91.5	305	21	AAO18536
9	532.5	91.5	305	21	AAO18536

10	532.5	91.5	305	21	AAO18536
11	532.5	91.5	305	21	AAO18536
12	532.5	90.8	338	19	AAO18536
13	528.5	90.8	338	21	AAO18536
14	528.5	90.8	338	21	AAO18536
15	528.5	90.8	338	21	AAO18536
16	528.5	90.8	338	21	AAO18536
17	526.5	90.5	338	23	AAO18536
18	526.5	90.5	338	23	AAO18536
19	526.5	90.5	338	24	AAO18536
20	522.5	89.8	111	15	AAO18536
21	522.5	89.8	111	15	AAO18536
22	522.5	89.8	111	15	AAO18536
23	519.5	89.3	111	10	AAO18536
24	519.5	89.3	111	23	AAO18536
25	519.5	89.3	111	23	AAO18536
26	515.5	88.6	113	22	AAO18536
27	515.5	88.6	113	22	AAO18536
28	515.5	88.6	113	22	AAO18536
29	511.5	87.9	131	11	AAO18536
30	503.5	86.5	106	14	AAO18536
31	503.5	86.5	106	21	AAO18536
32	498.5	85.7	103	21	AAO18536
33	498.5	85.7	103	21	AAO18536
34	491.5	84.5	111	14	AAO18536
35	491.5	84.5	111	14	AAO18536
36	487.5	83.8	120	15	AAO18536
37	487.5	83.8	218	24	AAO18536
38	487.5	83.8	218	24	AAO18536
39	487.5	83.8	238	19	AAO18536
40	487.5	83.8	238	21	AAO18536
41	487.5	83.8	238	21	AAO18536
42	487.5	83.8	238	23	AAO18536
43	485.5	83.4	111	20	AAO18536
44	485.5	83.4	111	22	AAO18536
45	476.5	81.9	238	19	AAO18536

ALIGNMENTS

RESULT 1  
AAO18536  
ID AAO18536 standard; Protein; 110 AA.  
AC AAO18536;  
DT 11-OCT-2002 (first entry)  
DE Murine Mab 1F7 light chain.  
KW Mouse; 1F7; antibody; immune modulator; anti-HIV antibody; CDR; complementarity determining region; framework-determining region; FR; heavy chain; light chain; HIV infection.  
OS Mus sp.  
PN WO200255668-A2.  
PD 18-JUL-2002.  
PF 11-JAN-2002; 2002WO-US00927.  
PR 11-JAN-2001; 2001US-0759112.  
(IMMP-) IMMOPHERON INC.  
PI Muller S, Kohler H;  
XX WPI; 2002-590668/63.  
XX N-PSDB; AAL48661.  
XX New polynucleotide encoding a complementarity- or framework-determining

PT region of an anti-idiotypic antibody that binds to human or primate  
 PT anti-human immunodeficiency virus (HIV) antibodies, for use in  
 PT vaccines against HIV -  
 XX  
 PS Claim 9; Page 23-24; 27pp; English.  
 XX  
 CC The present invention relates to coding sequences of the murine 1F7  
 CC anti-idiotypic antibody complementarity-determining region (CDR) or  
 CC framework-determining region (FR). The antibody binds to human or primate  
 CC anti-human immunodeficiency virus (HIV) antibodies and can be used in the  
 CC treatment of HIV infection. The present sequence is the 1F7 light chain.  
 XX  
 SQ Sequence 110 AA;

Query Match 100.0%; Score 582; DB 23; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-42;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSVVDYDGSYMWYQKPGQPPKLLTYAASNLESG 60  
 DB 1 DIVLTNSPASLAVSLGQRATISCKASQSVVDYDGSYMWYQKPGQPPKLLTYAASNLESG 60  
 QY 61 IPARESGSGSGTDFTLNHPVEEEDATYYCQNCNEDPPTFGAGTKLELK 110  
 DB 61 IPARESGSGSGTDFTLNHPVEEEDATYYCQNCNEDPPTFGAGTKLELK 110

RESULT 2  
 AAR70189  
 ID AAR70189 standard; Protein; 132 AA.  
 AC AAR70189;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 20-SEP-1995 (first entry)  
 XX  
 DE Mouse MAb 3B9 light chain.  
 XX  
 KW Chimeric antibody; humanized antibody; antibody engineering;  
 KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy.  
 XX

OS Mus sp.  
 FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT Region 44..58  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FT Region 74..80  
 FT /label= CDR  
 FT /note= "complementarity determining region"  
 FT Region 113..121  
 FT /label= CDR  
 FT /note= "complementarity determining region"

XX WO9507301-A1.  
 XX 16-MAR-1995.  
 XX 07-SEP-1994; 94WO-US10308.  
 XX  
 PR 07-SEP-1993; 93US-0117366.  
 PR 14-OCT-1993; 93US-0136783.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Gross MS, Holmes SD, Sylvester DR;  
 XX WPI; 1995-123387/16.  
 DR N-PSDB; AAQ83490.  
 XX

PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IGE-mediated allergic conditions  
 XX  
 PS Disclosure; Fig.1; 97pp; English.  
 XX  
 CC Spleen cells from mice immunized with human IL-4 were used to prepare  
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
 CC chains were cloned into pGEM7f+ and transformed into E. coli  
 CC DH5-alpha. The clones were sequenced (AAQ83490-91), and used for  
 CC antibody engineering.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 132 AA;  
 Query Match 92.4%; Score 537.5; DB 16; Length 132;  
 Best Local Similarity 93.7%; Pred. No. 1e-38;  
 Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSVVDYDGSYMWYQKPGQPPKLLTYAASNLES 59  
 DB 21 DIVLTQSPASLAVSLGQRATISCKASQSVVDYDGSYMWYQKPGQPPKLLTYAASNLES 80  
 QY 60 GIPARESGSGSGTDFTLNHPVEEEDATYYCQNCNEDPPTFGAGTKLELK 110  
 DB 81 GIPARESGSGSGTDFTLNHPVEEEDATYYCQNCNEDPPTFGAGTKLEIK 131

RESULT 3  
 AAY23767  
 ID AAY23767 standard; Protein; 132 AA.  
 AC AAY23767;  
 XX  
 DT 13-SEP-1999 (first entry)  
 XX  
 DE Light chain variable region of murine IL-4 antibody 3B9.  
 XX  
 KW Light chain variable region; interleukin-4; IL-4; antibody 3B9;  
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;  
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;  
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;  
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;  
 KW allergy.  
 XX  
 OS Mus sp.  
 XX US5928904-A.  
 XX 27-JUL-1999.  
 XX 07-JUN-1995; 95US-0483632.  
 XX 07-JUN-1995; 95US-0483632.  
 XX 07-SEP-1993; 93US-0117366.  
 XX 14-OCT-1993; 93US-0136783.  
 XX 07-SEP-1994; 94WO-US10308.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Gross MS, Holmes SD, Sylvester DR;  
 XX WPI; 1999-429500/36.  
 DR N-PSDB; AAQ85884.  
 XX  
 PT New DNA molecules encoding recombinant antibodies useful for  
 PT treating IL4-mediated conditions  
 XX  
 PS Example 3; Fig 1; 50pp; English.  
 XX  
 CC The present sequence represents the light chain variable region of

CC murine interleukin-4 (IL-4) antibody 3B9. The sequences are used  
 CC in the production of chimeric and humanised IL-4 monoclonal antibodies.  
 CC The antibodies of the invention are used in therapeutic and  
 CC pharmaceutical compositions for treating IL-4 mediated and  
 CC immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis,  
 CC conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock,  
 CC rheumatoid arthritis, host-versus-graft disease and renal disease.  
 CC They are also useful in the diagnosis of an allergy or condition  
 CC associated with excess IL-4 production through the measurement e.g. by  
 CC ELISA of circulating endogenous IL-4 levels in humans.

XX SQ Sequence 132 AA;  
 Query Match 92.4%; Score 537.5; DB 20; Length 132;  
 Best Local Similarity 93.7%; Pred. No. 1e-38; Indels 1; Gaps 1;  
 Matches 104; Conservative 1; Mismatches 5;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNLES 59  
 |||||  
 Db 21 DIVLTQSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNLES 80  
 |||||

QY 60 GIPARFSGSGTGDTFLNIHPVEEEDAATYYCOLCNEDEPPTFGAGTKLELK 110  
 |||||  
 Db 81 GIPARFSGSGTGDTFLNIHPVEEEDAATYYCQSNEDPPTFGGKTLEIK 131  
 |||||

RESULT 4  
 AAY18120  
 ID AAY18120 standard; Protein; 132 AA.  
 AC AAY18120;  
 XX  
 XX 11-AUG-1999 (first entry)  
 DE Light chain sequence for murine 3B9 antibody.  
 XX  
 XX Antibody; interleukin-4; IL4; immunoglobulin E; IGE mediated disease;  
 XX allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;  
 XX atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;  
 XX autoimmune disease; graft versus host disease.  
 XX Mus sp.  
 XX US5914110-A.  
 XX  
 XX 22-JUN-1999.  
 XX  
 XX 07-JUN-1995; 95US-0483636.  
 XX  
 XX 07-JUN-1995; 95US-0483636.  
 XX 07-SEP-1993; 93US-0117366.  
 XX 14-OCT-1993; 93US-0136783.  
 XX 07-SEP-1994; 94WO-US10308.  
 XX (SMIX ) SMITHKLINE BEECHAM CORP.  
 XX (SMIX ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Gross MS, Holmes SD, Sylvester DR;  
 XX WPI; 1999-370482/31.  
 XX N-PSDB; AAX79519.  
 XX  
 XX Recombinant IL4 antibodies  
 XX  
 XX Claim 24; Fig 1; 50pp; English.  
 XX  
 XX This sequence represents the light chain of the murine 3B9  
 XX antibody of the invention. The antibody is a chimeric or  
 XX humanised interleukin-4 (IL4) monoclonal antibody for the treatment of  
 XX immunoglobulin E (IGE) mediated diseases. The antibodies are useful for  
 XX the treatment of allergic disorders such as allergic rhinitis,  
 XX conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.  
 XX The antibodies are also useful for regulating B and T cell proliferation

CC and as such are useful in the treatment of autoimmune diseases and graft  
 CC versus host disease.  
 XX SQ Sequence 132 AA;  
 Query Match 92.4%; Score 537.5; DB 20; Length 132;  
 Best Local Similarity 93.7%; Pred. No. 1e-38; Indels 1; Gaps 1;  
 Matches 104; Conservative 1; Mismatches 5;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNLES 59  
 |||||  
 Db 21 DIVLTQSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNLES 80  
 |||||

QY 60 GIPARFSGSGTGDTFLNIHPVEEEDAATYYCOLCNEDEPPTFGAGTKLELK 110  
 |||||  
 Db 81 GIPARFSGSGTGDTFLNIHPVEEEDAATYYCQSNEDPPTFGGKTLEIK 131  
 |||||

RESULT 5  
 AAY59267  
 ID AAY59267 standard; protein; 111 AA.  
 AC AAY59267;  
 XX  
 XX 17-APR-2000 (first entry)  
 DE Antibody 4H5 L chain fragment.  
 XX  
 XX CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX Mus sp.  
 XX JPI1332563-A.  
 XX  
 XX 07-DEC-1999.  
 XX  
 XX 26-MAY-1998; 98JP-0163034.  
 XX  
 XX 26-MAY-1998; 98JP-0163034.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 XX WPI; 2000-091351/08.  
 XX N-PSDB; AAZ58690.  
 XX  
 XX An antibody and the nucleic acid coding the antibody -  
 XX  
 XX Disclosure; Page 22-23; 25pp; Japanese.  
 XX  
 XX The invention provides an antibody having affinity to CD4 antigen. The  
 XX anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 XX application for drugs. It is highly safe in human dose. The present  
 XX sequence represents a L chain fragment of the antibody 4H5.

XX SQ Sequence 111 AA;  
 Query Match 91.5%; Score 532.5; DB 21; Length 111;  
 Best Local Similarity 92.8%; Pred. No. 2.3e-38;  
 Matches 103; Conservative 2; Mismatches 5;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNLES 59  
 |||||  
 Db 1 DIVLTQSPASLAVSLGQRATISCKASQSYDYGDSYM-WYQKPGQPPKLLTYAASNLES 60  
 |||||

QY 60 GIPARFSGSGTGDTFLNIHPVEEEDAATYYCOLCNEDEPPTFGAGTKLELK 110  
 |||||  
 Db 61 GIPARFSGSGTGDTFLNIHPVEEEDAATYYCQSNEDPPTFGGKTLEIK 111  
 |||||

RESULT 6  
 AAY51144  
 ID AAY51144 standard; Protein; 111 AA.  
 XX

AC AAY51144;  
 DT 31-MAR-2000 (first entry)  
 XX Murine derived protein fragment #8.  
 DE  
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 XX  
 OS Mus sp.  
 XX WO9961629-A1.  
 PN  
 PD 02-DEC-1999.  
 XX  
 XX 24-MAY-1999; 99WO-JP02711.  
 XX 25-MAY-1998; 98JP-0159957.  
 XX 26-MAY-1998; 98JP-0163023.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 PA (ASAH ) ASAH MEDICAL CO LTD.  
 XX  
 PI Ono M, Soka T, Morimoto I, Miyamura K;  
 XX WPI; 2000-086720/07.  
 DR  
 XX 25-MAY-1998; 98JP-0159957.  
 PR 26-MAY-1998; 98JP-0163023.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 PA (ASAH ) ASAH MEDICAL CO LTD.  
 XX  
 PI Ono M, Soka T, Morimoto I, Miyamura K;  
 XX WPI; 2000-086720/07.  
 DR  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 XX  
 PS Disclosure; Page 95; 11pp; Japanese.  
 XX  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 SQ Sequence 111 AA;  
 Query Match 91.5%; Score 532.5; DB 21; Length 111;  
 Best Local Similarity 92.8%; Pred. No. 2.3e-38;  
 Matches 103; Conservative 5; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59  
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPPKLLTYAASNLES 60  
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLCNEDEPPTFGAGTKLELK 110  
 DB 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQSSSEDPPTFGGSKLEIK 111  
 RESULT 7  
 AAY51146  
 ID AAY51146 standard; Protein; 111 AA.  
 XX  
 AC AAY51146;  
 XX  
 DT 31-MAR-2000 (first entry)  
 XX Murine derived protein fragment #8.  
 DE  
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 XX

OS Mus sp.  
 XX WO9961629-A1.  
 PN  
 PD 02-DEC-1999.  
 XX  
 XX 24-MAY-1999; 99WO-JP02711.  
 XX 25-MAY-1998; 98JP-0159957.  
 XX 26-MAY-1998; 98JP-0163023.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 PA (ASAH ) ASAH MEDICAL CO LTD.  
 XX  
 PI Ono M, Soka T, Morimoto I, Miyamura K;  
 XX WPI; 2000-086720/07.  
 DR N-PSDB; AA244232.  
 XX  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 XX  
 PS Disclosure; Page 97-98; 11pp; Japanese.  
 XX  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 SQ Sequence 111 AA;  
 Query Match 91.5%; Score 532.5; DB 21; Length 111;  
 Best Local Similarity 92.8%; Pred. No. 2.3e-38;  
 Matches 103; Conservative 5; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59  
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPPKLLTYAASNLES 60  
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLCNEDEPPTFGAGTKLELK 110  
 DB 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQSSSEDPPTFGGSKLEIK 111  
 RESULT 8  
 AAY59264  
 ID AAY59264 standard; protein; 305 AA.  
 XX  
 AC AAY59264;  
 XX  
 DT 17-APR-2000 (first entry)  
 XX  
 XX Antibody 4H5 H chain sequence.  
 XX  
 KW CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX  
 OS Mus sp.  
 XX JP11332563-A.  
 PN  
 PD 07-DEC-1999.  
 XX  
 XX 26-MAY-1998; 98JP-0163034.  
 XX 26-MAY-1998; 98JP-0163034.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 PA



XX  
DR WPI; 2000-091351/08.  
DR N-PSDB; AA258663.  
XX  
PT An antibody and the nucleic acid coding the antibody -  
XX  
PS Disclosure; Page 16-17; 25pp; Japanese.  
XX  
CC The invention provides an antibody having affinity to CD4 antigen. The  
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
CC application for drugs. It is highly safe in human dose. The present  
CC sequence represents the H chain sequence of the antibody 4H5.  
XX  
SQ Sequence 305 AA;  
  
Query Match 91.5%; Score 532.5; DB 21; Length 305;  
Best Local Similarity 92.8%; Pred. No. 6.3e-38;  
Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;  
  
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSTM-WYQKPGQPPKLLTYAASNL 59  
Db 23 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSTMWYQKPGQPPKLLTYAASNL 82  
  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQCNEDPPTFGAGTKLELK 110  
Db 83 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSEDPTFGGKLEIK 133  
  
RESULT 9  
AA59265  
ID AAY59265 standard; protein; 305 AA.  
AC AAY59265;  
XX  
DT 17-APR-2000 (first entry)  
DE Antibody 4H5 L chain sequence.  
XX  
KW CD4 antigen; anti-human; antibody; 4H5; drug.  
XX  
OS Mus sp.  
XX  
PN JP11332563-A.  
PD 07-DEC-1999.  
XX  
PF 26-MAY-1998; 98JP-0163034.  
XX  
PR 26-MAY-1998; 98JP-0163034.  
XX  
PA (ASAH ) ASAH KASEI KOGYO KK.  
XX  
DR WPI; 2000-091351/08.  
DR N-PSDB; AA258664.  
XX  
PT An antibody and the nucleic acid coding the antibody -  
XX  
PS Disclosure; Page 17-18; 25pp; Japanese.  
XX  
CC The invention provides an antibody having affinity to CD4 antigen. The  
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
CC application for drugs. It is highly safe in human dose. The present  
CC sequence represents the L chain sequence of the antibody 4H5.  
XX  
SQ Sequence 305 AA;  
  
Query Match 91.5%; Score 532.5; DB 21; Length 305;  
Best Local Similarity 92.8%; Pred. No. 6.3e-38;  
Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;  
  
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSTM-WYQKPGQPPKLLTYAASNL 59  
Db 156 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSTMWYQKPGQPPKLLTYAASNL 215  
  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQCNEDPPTFGAGTKLELK 110  
Db 83 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSEDPTFGGKLEIK 133  
  
RESULT 10  
AA51141  
ID AAY51141 standard; Protein; 305 AA.  
XX  
AC AAY51141;  
XX  
DT 31-MAR-2000 (first entry)  
XX  
DE Murine derived protein fragment #3.  
XX  
KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
KW HIV infection; autoimmune disease; murine.  
XX  
OS Mus sp.  
XX  
FN WO9961629-A1.  
XX  
PD 02-DEC-1999.  
XX  
PF 24-MAY-1999; 99WO-JP02711.  
XX  
PR 25-MAY-1998; 98JP-0159957.  
XX  
PR 26-MAY-1998; 98JP-0163023.  
XX  
PA (ASAH ) ASAH KASEI KOGYO KK.  
XX  
PA (ASAH ) ASAH MEDICAL CO LTD.  
XX  
PI Ono M, Soka T, Morimoto I, Miyamura K;  
XX  
DR WPI; 2000-086720/07.  
DR N-PSDB; AA244205.  
XX  
PT Devices containing antibodies recognising CD4 or CD34 and their use for  
PT the separation of CD4 or CD34 positive cells -  
XX  
FS Claim 22; Page 80-82; 11pp; Japanese.  
XX  
CC This invention describes a novel device (I) for separating cluster  
CC differentiation (CD)-positive cells using a recombinant (chimeric or  
CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
CC for the separation of CD4 or CD34 positive cells, which is useful for  
CC the collection of hematopoietic undifferentiated cells, elimination of  
CC lymphocytes from cells to be used in bone marrow transplantation, the  
CC detection of leukemic cells and the production of medicinal  
CC compositions for the treatment of HIV infection and autoimmune diseases.  
CC This sequence represents a murine derived protein fragment which is used  
CC to illustrate the method of the invention.  
XX  
SQ Sequence 305 AA;  
  
Query Match 91.5%; Score 532.5; DB 21; Length 305;  
Best Local Similarity 92.8%; Pred. No. 6.3e-38;  
Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;  
  
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSTM-WYQKPGQPPKLLTYAASNL 59  
Db 23 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSTMWYQKPGQPPKLLTYAASNL 82  
  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQCNEDPPTFGAGTKLELK 110  
Db 83 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSEDPTFGGKLEIK 133  
  
RESULT 11  
AA51142  
ID AAY51142 standard; Protein; 305 AA.

AC AAY51142;  
 DT 31-MAR-2000 (first entry)  
 DE Murine derived protein fragment #4.  
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 OS Mus sp.  
 PN WO9961629-A1.  
 PD 02-DEC-1999.  
 XX 24-MAY-1999; 99WO-JP02711.  
 XX 25-MAY-1998; 98JP-0159957.  
 XX 26-MAY-1998; 98JP-0163023.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 XX (ASAH ) ASAH MEDICAL CO LTD.  
 XX Ono M, Soka T, Morimoto I, Miyamura K;  
 XX WPI: 2000-086720/07.  
 XX N-PSDB; AA244206.  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 XX the separation of CD4 or CD34 positive cells -  
 XX Claim 22; Page 82-84; 111pp; Japanese.  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX Sequence 305 AA;  
 SQ Query Match 91.5%; Score 532.5; DB 21; Length 305;  
 Best Local Similarity 92.8%; Pred. No. 6.3e-38;  
 Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNL 59  
 DB 156 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSYMWYQKPGQPPKLLTYAASNL 215  
 QY 60 GIPARFSGSGSDTFLNIHPVEEEDAAITYCQLNEDPPTFGAGTKLEIX 110  
 DB 216 GIPARFSGSGSDTFLNIHPVEEEDAAITYCQSSDPTFGGTKLEIX 266  
 RESULT 12  
 ID AAW83042  
 XX AAW83042 standard; Protein; 238 AA.  
 AC AAW83042;  
 XX 25-MAR-2003 (updated)  
 DT 15-MAR-1999 (first entry)  
 DE Anti-Fas MAb HFE7A light chain.  
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW

KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy; complementarity determining region;  
 CDR.  
 XX  
 XX Mus musculus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 XX Peptide 1..20  
 FT /label= sig\_peptide  
 FT Protein 21..238  
 FT /label= Mat\_protein  
 FT Region 21..131  
 FT /label= variable  
 FT Region 132..238  
 FT /label= Constant  
 FT Region 44..58  
 FT /label= CDR L1  
 FT /note= "claim 9"  
 FT Region 74..80  
 FT /label= CDR L2  
 FT /note= "claim 9"  
 FT Region 113..121  
 FT /label= CDR L3  
 FT /note= "claim 9"  
 XX  
 XX AU9859701-A.  
 XX  
 XX 08-OCT-1998.  
 XX 30-MAR-1998; 98AU-0059701.  
 XX 08-OCT-1997; 97JP-0276064.  
 XX 01-APR-1997; 97JP-0082953.  
 XX 25-JUN-1997; 97JP-0169088.  
 XX (SANY ) SANKYO CO LTD.  
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 XX Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 XX WPI: 1998-543440/01.  
 XX N-PSDB; AAV70130.  
 XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 XX used to evaluate drugs in animal models and to treat Fas-associated  
 XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 XX myocarditis, hepatitis and AIDS  
 XX Reference Example 4; Page 189-190; 292pp; English.  
 XX This is the amino acid of the light chain of murine anti-human Fas  
 XX monoclonal antibody HFE7A. cDNA (see AAV70130) encoding the light  
 XX chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)  
 XX RNA by RT-PCR (see AAV70127-28). The invention provides humanised  
 XX HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These  
 XX antibodies are capable of inducing apoptosis in abnormal cells  
 XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal  
 XX cells. They are used to evaluate, in animal models, treatments of  
 XX diseases that involve Fas/Fas ligand interactions, and also to treat  
 XX such diseases, including autoimmune disease (e.g. systemic lupus  
 XX erythematosus, Hashimoto's disease, graft versus host disease,  
 XX Sjogren syndrome, pernicious anaemia, Addison's disease,  
 XX scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid  
 XX arthritis, autoimmune haemolytic anaemia, sterility, myasthenia  
 XX gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura  
 CC

CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
 CC (Updated on 25-MAR-2003 to correct DR field.)  
 XX  
 SQ Sequence 238 AA;  
 Query Match 90.8%; Score 528.5; DB 19; Length 238;  
 Best Local Similarity 92.8%; Pred. No. 1.1e-37;  
 Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59  
 DB 21 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 80  
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYVCOQSNEDPRTFGGKLEIK 110  
 DB 81 GIPARFSGSGGTDFTLNHPVEEEDAAATYVCOQSNEDPRTFGGKLEIK 131  
 RESULT 13  
 AAB14748  
 ID AAB14748 standard; Protein; 238 AA.  
 XX  
 AC AAB14748;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE Mouse anti-Fas antibody HFE7A light chain.  
 XX  
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; complementarity determining region; CDR; human Fas;  
 KW Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; Graft rejection; light chain.  
 XX  
 OS Mus musculus.  
 XX  
 PN JP2000169393-A.  
 XX  
 PD 20-JUN-2000.  
 XX  
 PF 30-SEP-1999; 99JP-0278301.  
 XX  
 PR 30-SEP-1998; 98JP-0276883.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 WPI: 2000-485645/43.  
 DR N-PSDB; AAB14748.  
 XX  
 PT Preventive or treating agent for the diseases caused by an abnormality  
 in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 anti-Fas antibody  
 XX  
 PS Example 4; Page 70; 139pp; Japanese.  
 XX  
 CC The invention relates to compositions for the prevention or treatment  
 of diseases caused by an abnormality in the Fas/Fas ligand system  
 containing an anti-Fas antibody as the active component. The anti-Fas  
 antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 or a humanised version of HFE7A containing identical CDRs  
 (complementarity determining regions) to antibody HFE7A. Via its  
 interaction with Fas, the antibody of the invention acts as a modulator  
 of apoptosis. The compositions of the invention may therefore be used in  
 the treatment or prevention of conditions such as autoimmune diseases,  
 allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 and organ graft rejection. The present sequence represents the  
 light chain of the murine anti-human Fas monoclonal antibody HFE7A,  
 which is produced by hybridoma HFE7A (FERM-BP-5828).  
 XX

SQ Sequence 238 AA;  
 Query Match 90.8%; Score 528.5; DB 21; Length 238;  
 Best Local Similarity 92.8%; Pred. No. 1.1e-37;  
 Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 59  
 DB 21 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNLES 80  
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYVCOQSNEDPRTFGGKLEIK 110  
 DB 81 GIPARFSGSGGTDFTLNHPVEEEDAAATYVCOQSNEDPRTFGGKLEIK 131  
 RESULT 14  
 AAW90898  
 ID AAW90898 standard; Protein; 238 AA.  
 XX  
 AC AAW90898;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Murine anti-Fas antibody HFE7A light chain protein.  
 XX  
 KW Fas: antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Godpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Mus musculus.  
 XX  
 PN EP990663-A2.  
 XX  
 PD 05-APR-2000.  
 XX  
 PF 29-SEP-1999; 99EP-0307711.  
 XX  
 PR 30-SEP-1998; 98JP-0276881.  
 XX  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 WPI: 2000-258930/23.  
 DR N-PSDB; AAW1547.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 inflammatory or autoimmune disease, induces apoptosis selectively in  
 cells with abnormal Fas-Fas ligand systems  
 XX  
 PS Example reference 4; Page 104; 263pp; English.  
 XX  
 CC This invention describes a novel humanized anti-Fas antibody-like  
 molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 ligand system, by binding to Fas on the cell surface, and prevents  
 apoptosis in cells with a normal system, by inhibiting binding between  
 Fas and its ligand. The products of the invention have anti-inflammatory,  
 anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 apoptosis by binding to cell surface Fas or inhibit it by competitive  
 inhibition of ligand binding. (I) are used to treat and/or prevent  
 diseases associated with the Fas/Fas ligand system, especially systemic

CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a murine anti-Fas monoclonal antibody HPE7A light chain described in the  
 CC method of the invention.  
 XX  
 SQ Sequence 238 AA;

Query Match 90.8%; Score 528.5; DB 21; Length 238;  
 Best Local Similarity 92.8%; Pred. No. 1.1e-37;  
 Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGORATISCKASQSVYDGDSTM-WYQKPGQPPKLLTYAASNLES 59  
 DB 21 DIVLTQSPASLAVSLGORATISCKASQSVYDGDSTMWYQKPGQPPKLLTYAASNLES 80  
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQNSNEDPRTFGGKLEIK 110  
 DB 81 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQNSNEDPRTFGGKLEIK 131

RESULT 15  
 ABB74867  
 ID ABB74867 standard; Peptide; 238 AA.  
 XX AC ABB74867;  
 DT 26-APR-2002 (first entry)  
 XX Humanised anti-Fas antibody related peptide SEQ ID NO 33.  
 DE Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;  
 KW light chain subunit; apoptosis; immunosuppressive; antiallergic;  
 KW autoimmune disease; allergy; atopic.  
 XX OS Homo sapiens.  
 XX JP2001342148-A.  
 XX PD 11-DEC-2001.  
 XX PF 28-MAR-2001; 2001JP-0093106.  
 XX PR 29-MAR-2000; 2000JP-0090918.  
 XX (SANYO) SANKYO CO LTD.  
 XX PA WPI; 2002-145113/19.  
 XX DR Drug containing humanised anti-Fas antibody, used for preventing and  
 XX PT treating autoimmune diseases, allergy, and atopy -  
 XX PS Example 6 (Preparatory); Page 26; 194pp; Japanese.  
 XX

The invention relates to a preventive or treating agent for diseases  
 caused by abnormality in Fas/Fas ligand system containing as the active  
 component an antibody having as the light chain subunit a polypeptide  
 containing residues 1-218 of one of 3, 239 residue amino acid sequences,  
 or residues 1-451 of one of 3, 470 residue amino acid sequences, all  
 fully defined in the specification and having an activity of combining  
 specifically with mammalian Fas and an activity of inducing apoptosis  
 in a cell expressing Fas. The agent has immunosuppressive and  
 CC antiallergic activity and is used for preventing and treating autoimmune

CC diseases, allergy, atopy and others. The present sequence is that of a  
 CC peptide, useful to the invention.  
 XX  
 SQ Sequence 238 AA;  
 Query Match 90.8%; Score 528.5; DB 23; Length 238;  
 Best Local Similarity 92.8%; Pred. No. 1.1e-37;  
 Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGORATISCKASQSVYDGDSTM-WYQKPGQPPKLLTYAASNLES 59  
 DB 21 DIVLTQSPASLAVSLGORATISCKASQSVYDGDSTMWYQKPGQPPKLLTYAASNLES 80  
 QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQNSNEDPRTFGGKLEIK 110  
 DB 81 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQNSNEDPRTFGGKLEIK 131

Search completed: January 14, 2004, 19:11:26  
 Job time : 35.8095 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 19:02:07 ; Search time 14.7619 Seconds  
(without alignments)  
716.612 Million cell updates/sec

Title: US-09-759-112A-24  
Perfect score: 582  
Sequence: 1 DIVLTNSPASLAVSLQGRAT.....COLCNEDEPTFGAGTKLELK 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76.\*  
1: Piri.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533.5	91.7	111	1 KWS83	Ig kappa chain V r
2	527.5	90.6	111	1 KWS43	Ig kappa chain V r
3	523.5	89.9	111	1 KWS08	Ig kappa chain V r
4	521.5	89.6	112	1 S19971	Ig kappa chain V r
5	521.5	89.6	131	2 PH1226	Ig kappa chain pre
6	520.5	89.4	111	1 KWS69	Ig kappa chain V r
7	505	86.8	110	1 KWS10	Ig kappa chain V r
8	503.5	86.5	111	1 KWSCL	Ig kappa chain V r
9	502.5	86.3	112	2 S19976	Ig kappa chain V r
10	485.5	83.4	112	2 S19972	Ig kappa chain V r
11	476.5	81.9	111	2 S09966	Ig kappa chain V r
12	473.5	81.4	111	1 KWS75	Ig kappa chain V-J
13	470.5	80.8	111	1 KWS40	Ig kappa chain V r
14	468.5	80.5	111	1 KWS84	Ig kappa chain V r
15	457.5	78.6	112	2 S45715	Ig kappa chain V r
16	455.5	78.3	111	1 KWS37	Ig kappa chain V r
17	454.5	78.1	111	1 KWS85	Ig kappa chain V r
18	452.5	77.7	131	2 S5027	Ig kappa chain V r
19	451.5	77.6	210	2 A56169	Ig light chain pre
20	449.5	77.2	218	2 JCS810	Ig kappa chain V r
21	448.5	77.1	131	1 KWSM6	monoclonal antibody
22	445.5	76.5	218	2 S68241	Ig kappa chain pre
23	442.5	76.0	115	2 S63596	Ig kappa chain V r
24	441.5	75.9	93	2 A38601	Ig kappa chain V r
25	438.5	75.3	111	2 S09963	Ig kappa chain V r
26	438.5	75.3	111	2 D45722	Ig kappa chain V-J
27	432.5	74.3	111	1 KWS80	anti-glycoprotein
28	430.5	74.0	107	2 S26343	Ig kappa chain V r
29	430.5	74.0	107	2 S26344	Ig kappa chain V r

ALIGNMENTS

RESULT 1

KWS83  
Ig kappa chain V region (PC7183) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
C:Accession: B01937; A01937  
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152; PMID:103003  
A:Accession: B01937  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 91.7%; Score 533.5; DB 1; Length 111;  
Best Local Similarity 94.6%; Pred. No. 2.6e-41;  
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
Qy 1 DIVLTNSPASLAVSLQGRATISCKASQSDYDGDSTVWYQKPGQPPKLLTYAASNLSS 59  
Db 1 DIVLTNSPASLAVSLQGRATISCKASQSDYDGDSTVWYQKPGQPPKLLTYAASNLSS 60  
Qy 60 GIPARFSGSGGDTFTLNHPVEEEDAAATYQCNEDEPTFGAGTKLELK 110  
Db 61 GIPARFSGSGGDTFTLNHPVEEEDAAATYQCNEDEPTFGAGTKLELK 111

RESULT 2

KWS43  
Ig kappa chain V region (PC7043) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192  
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152; PMID:103003  
A:Accession: A01937  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.  
Eur. J. Immunol. 23, 2503-2510, 1993  
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spe  
A:Reference number: S42176; MUID:94009207; PMID:7691608  
A:Accession: S42187  
A:Molecule type: DNA

A:Residues: 10-99 <MO>  
 A:CROSS-references: EMBL:225444; NID:9407832; PIDN:CAA80931.1; PID:9407833  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42194  
 A:Molecule type: DNA  
 A:Residues: 12-99 <MO>  
 A:CROSS-references: EMBL:225458; NID:9407844; PIDN:CAA80945.1; PID:9407845  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42190  
 A:Molecule type: DNA  
 A:Residues: 13-99 <MO>  
 A:CROSS-references: EMBL:225450; NID:9407838; PIDN:CAA80937.1; PID:9407839  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42189  
 A:Molecule type: DNA  
 A:Residues: 15-99 <MO>  
 A:CROSS-references: EMBL:225448; NID:9407836; PIDN:CAA80935.1; PID:9407837  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42188  
 A:Molecule type: DNA  
 A:Residues: 12-99 <MO>  
 A:CROSS-references: EMBL:225446; NID:9407834; PIDN:CAA80933.1; PID:9407835  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42191  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MO>  
 A:CROSS-references: EMBL:225452; NID:9407840; PIDN:CAA80939.1; PID:9407841  
 A>Note: V-kappa-21E; anti-collagen  
 A:Accession: S42192  
 A:Molecule type: DNA  
 A:Residues: 10-99 <MO>  
 A:CROSS-references: EMBL:225454; NID:9407842; PIDN:CAA80941.1; PID:9407843  
 A>Note: V-kappa-21E; anti-collagen  
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status Predicted

Query Match 90.6%; Score 527.5; DB 1; Length 111;  
 Best Local Similarity 92.8%; Pred. No. 8.9e-41;  
 Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDYSYM-WYQKPGQPPKLLITYAASNLES 59  
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDYSYM-WYQKPGQPPKLLITYAASNLES 60  
 QY 60 GIPARFSGSGGTDFLTNIHPVEEDATYYCQCNEDPPTFGAGTKLEIK 110  
 DB 61 GIPARFSGSGGTDFLTNIHPVEEDATYYCQCNEDPPTFGAGTKLEIK 111

RESULT 3  
 IG kappa chain V region (PC308) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
 C:Accession: C01937; A01937  
 R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
 Nature 276, 785-790, 1978  
 A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
 A:Reference number: A93204; MUID:79073152; PMID:103003  
 A:Accession: C01937  
 A:Molecule type: protein  
 A:Residues: 1-111 <WEI>  
 A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status Predicted

Query Match 89.9%; Score 523.5; DB 1; Length 111;  
 Best Local Similarity 91.9%; Pred. No. 2e-40;  
 Matches 102; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDYSYM-WYQKPGQPPKLLITYAASNLES 59  
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDYSYM-WYQKPGQPPKLLITYAASNLES 60  
 QY 60 GIPARFSGSGGTDFLTNIHPVEEDATYYCQCNEDPPTFGAGTKLEIK 110  
 DB 61 GIPARFSGSGGTDFLTNIHPVEEDATYYCQCNEDPPTFGAGTKLEIK 111

RESULT 4  
 S19971  
 IG kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S19971; S19973  
 R:Weissenhorn, W.; Rietmuller, G.; Weiss, E.M.; Rieber, E.P.  
 submitted to the EMBL Data Library, March 1992  
 A:Description: Structural characterization of CD4 mAb.  
 A:Reference number: S19963  
 A:Accession: S19971  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <WEI>  
 A:CROSS-references: EMBL:X65091; NID:952288; PIDN:CAA46219.1; PID:952289  
 A:Experimental source: clone M-T310  
 A:Accession: S19973  
 A:Molecule type: mRNA  
 A:Residues: 1-112 <WEI>  
 A:CROSS-references: EMBL:X65092; NID:952292; PIDN:CAA46220.1; PID:952293  
 A:Experimental source: M-T404  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 89.6%; Score 521.5; DB 2; Length 112;  
 Best Local Similarity 90.1%; Pred. No. 3.1e-40;  
 Matches 100; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDYSYM-WYQKPGQPPKLLITYAASNLES 59  
 DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDYSYM-WYQKPGQPPKLLITYAASNLES 60  
 QY 60 GIPARFSGSGGTDFLTNIHPVEEDATYYCQCNEDPPTFGAGTKLEIK 110  
 DB 61 GIPARFSGSGGTDFLTNIHPVEEDATYYCQCNEDPPTFGAGTKLEIK 111

RESULT 5  
 PH1226  
 IG kappa chain precursor V region (M-T310) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jan-2000  
 C:Accession: PH1226  
 R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenig, G.  
 Gene 121, 271-278, 1992  
 A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and CD8.  
 A:Reference number: PH1224; MUID:93077041; PMID:1446824  
 A:Accession: PH1226  
 A:Molecule type: mRNA  
 A:Residues: 1-131 <WEI>  
 A:CROSS-references: GB:S50265; NID:9260765; PIDN:AA24320.1; PID:9260766  
 A>Note: This mouse sequence was hybridized and fused with a human constant region gene.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-131/Product: Ig light chain V region #status predicted <MAT>  
 F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 89.6%; Score 521.5; DB 2; Length 131;  
 Best Local Similarity 90.1%; Pred. No. 3.6e-40;

```
Matches 100; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
QY 1 DIVLTNPASLAVSLGQRTATISCKASQSDYDGDSDYM-WYQKPGOPPKLLTYAASNLES 59
Db 21 DIVLTQSPASLPMISLQRTATISCKASQSLDYDGDSDYMWYQKPGOPPKLLTYAASNLES 80
QY 60 GIPARFSGSGSGDTFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEK 110
Db 81 GIPARFSGSGSGDTFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEK 131

RESULT 6
KWS69
Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: E01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
C:Accession: E01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 89.4%; Score 520.5; DB 1; Length 111;
Best Local Similarity 91.0%; Pred. No. 3.8e-40;
Matches 101; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
QY 1 DIVLTNPASLAVSLGQRTATISCKASQSDYDGDSDYM-WYQKPGOPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGQRTATISCKASQSDYDGDSDYMWYQKPGOPPKLLTYAASNLES 60
QY 60 GIPARFSGSGSGDTFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEK 110
Db 61 GIPARFSGSGSGDTFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEK 111

RESULT 7
KWS10
Ig kappa chain V region (PC7210) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: D01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
C:Accession: D01937
A:Molecule type: protein
A:Residues: 1-110 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 86.8%; Score 505; DB 1; Length 110;
Best Local Similarity 90.1%; Pred. No. 9.4e-39;
Matches 100; Conservative 4; Mismatches 5; Indels 2; Gaps 2;
QY 1 DIVLTNPASLAVSLGQRTATISCKASQSDYDGDSDYM-WYQKPGOPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGQRTATISCKASQSLDYDGDSDYMWYQKPGOPPKLLTYAASNLES 60
QY 60 GIPARFSGSGSGDTFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEK 110
```

```
Db 61 GIPARFSGSGSGDTFTLNHPVEEEDAATYYCHQ-SEDPWTFSGTKLEK 110

RESULT 8
KWSCL
Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
C:Accession: A01936
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related m
A:Reference number: A93822; MUID:79012520; PMID:99744
C:Accession: A01936
A:Molecule type: protein
A:Residues: 1-111 <MCK>
C:Comment: This chain was isolated from a myeloma protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 86.5%; Score 503.5; DB 1; Length 111;
Best Local Similarity 89.2%; Pred. No. 1.3e-38;
Matches 99; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
QY 1 DIVLTNPASLAVSLGQRTATISCKASQSDYDGDSDYM-WYQKPGOPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGQRTATISCKASQSDYDGDSDYMWYQKPGOPPKLLTYAASNLES 60
QY 60 GIPARFSGSGSGDTFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEK 110
Db 61 GIPARFSGSGSGDTFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEK 111

RESULT 9
S19976
Ig kappa chain V region (M-T413) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19976
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19976
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 86.3%; Score 502.5; DB 2; Length 112;
Best Local Similarity 88.3%; Pred. No. 1.6e-38;
Matches 98; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
QY 1 DIVLTNPASLAVSLGQRTATISCKASQSDYDGDSDYM-WYQKPGOPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGQRTATISCKASQSLDYDGDSDYMWYQKPGOPPKLLTYAASNLES 60
QY 60 GIPARFSGSGSGDTFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEK 110
Db 61 GIPARFSGSGSGDTFTLNHPVEEEDAATYYCQCNEDPPTFGAGTKLEK 111

RESULT 10
S19972
Ig kappa chain V region (M-T321) - mouse (fragment)
```

C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S19972  
R;Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A;Description: Structural characterization of CD4 mAb.  
A;Reference number: S19963  
A;Accession: S19972  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <WEI>  
A;Cross-references: EMBL:X65094; NID:G52290; PID:CAA46222.1; PID:G52291  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-94/Domain: immunoglobulin homology <IMM>  
  
Query Match 83.4%; Score 485.5; DB 2; Length 112;  
Best Local Similarity 85.6%; Pred. No. 5.5e-37;  
Matches 95; Conservative 6; Mismatches 9; Indels 1; Gaps 1;  
  
QY 1 DIVLTNSPASLAVSLGORATISCKASQSVYDGDSDYM-WYQKPGQPPKLLTYAASNL 59  
Db 1 DIVLTQSPASLAVSLGORATIFCRASQSVYDYNATSYMEWYQKPGQPPKLLTYAASNL 60  
  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDATYYCQNCNEDPPTFGAGTKLEK 110  
Db 61 GIPARFSGSGGTDFTLNHPVEEEDATYYCQNCNEDPPTFGAGTKLEK 111  
  
RESULT 11  
KWMS66  
Ig kappa chain V-J region (1E10) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 21-Jan-2000  
C;Accession: S03966  
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.  
Eur. J. Immunol. 20, 771-777, 1990  
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies  
A;Reference number: S03965; MUID:90269328; PMID:2347362  
A;Accession: S03966  
A;Molecule type: mRNA  
A;Residues: 1-111 <REI>  
A;Cross-references: EMBL:X51854; NID:G55397; PID:CAA36147.1; PID:G930231  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-94/Domain: immunoglobulin homology <IMM>  
  
Query Match 81.9%; Score 476.5; DB 2; Length 111;  
Best Local Similarity 84.7%; Pred. No. 3.5e-36;  
Matches 94; Conservative 1; Mismatches 15; Indels 1; Gaps 1;  
  
QY 1 DIVLTNSPASLAVSLGORATISCKASQSVYDGDSDYM-WYQKPGQPPKLLTYAASNL 59  
Db 1 DIVXTQSPAXLAXSLGORATISCKASXSVYDGDSDYMWYQKPPQPPKLLTYGASNL 60  
  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDATYYCQNCNEDPPTFGAGTKLEK 110  
Db 61 GIPARFSGSGGTDFTLNHPVEEEDATYYCQNCNEDPPTFGAGTKLEK 111  
  
RESULT 12  
KWMS75  
Ig kappa chain V region (PC7175) - mouse (tentative sequence)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 31-Mar-2000  
C;Accession: B01938; A01938  
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A;Reference number: A93204; MUID:79073152; PMID:103003  
A;Accession: B01938  
A;Molecule type: protein  
A;Residues: 1-111 <WEI>

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-94/Domain: immunoglobulin homology <IMM>  
F;23-92/Disulfide bonds: #status predicted  
  
Query Match 81.4%; Score 473.5; DB 1; Length 111;  
Best Local Similarity 85.6%; Pred. No. 6.6e-36;  
Matches 95; Conservative 3; Mismatches 12; Indels 1; Gaps 1;  
  
QY 1 DIVLTNSPASLAVSLGORATISCKASQSVYDGDSDYM-WYQKPGQPPKLLTYAASNL 59  
Db 1 DIVLTQSPASLAVSLGORATISCRASKSVTSYGYSYMEWYQKPGQPPKLLTYLASNL 60  
  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDATYYCQNCNEDPPTFGAGTKLEK 110  
Db 61 GVPARFSGSGGTDFTLNHPVEEEDATYYCQHSRELPLTFEGAGTKLEK 111  
  
RESULT 13  
KWMS40  
Ig kappa chain V region (PC7940) - mouse (tentative sequence)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 31-Mar-2000  
C;Accession: C01938; A01938  
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A;Reference number: A93204; MUID:79073152; PMID:103003  
A;Accession: C01938  
A;Molecule type: protein  
A;Residues: 1-111 <WEI>  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-94/Domain: immunoglobulin homology <IMM>  
F;23-92/Disulfide bonds: #status predicted  
  
Query Match 80.8%; Score 470.5; DB 1; Length 111;  
Best Local Similarity 83.8%; Pred. No. 1.2e-35;  
Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;  
  
QY 1 DIVLTNSPASLAVSLGORATISCKASQSVYDGDSDYM-WYQKPGQPPKLLTYAASNL 59  
Db 1 DIVLTQSPASLAVSLGORATISCRASKSVSAFGYSYMEWYQKPGQPPKLLTYLASNL 60  
  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDATYYCQNCNEDPPTFGAGTKLEK 110  
Db 61 GVPARFSGSGGTDFTLNHPVEEEDATYYCQHSRELPLTFEGAGTKLEK 111  
  
RESULT 14  
KWMS84  
Ig kappa chain V region (PC6684) - mouse (tentative sequence)  
C;Species: Mus musculus (house mouse)  
C;Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 31-Mar-2000  
C;Accession: A01938  
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A;Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A;Reference number: A93204; MUID:79073152; PMID:103003  
A;Accession: A01938  
A;Molecule type: protein  
A;Residues: 1-111 <WEI>  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;16-94/Domain: immunoglobulin homology <IMM>  
F;23-92/Disulfide bonds: #status predicted



```
Query Match      80.5%; Score 468.5; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 1.9e-35;
Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSYVDYDGDSYM-WYQOKPGQPPKLLTYAASNLES 59
   |||||
Db 1 DIVLTQSPASLAVSLGORATISCRASKSVSTSGSYMHWYQOKPGQPPKLLIYLASNLES 60
   |||||

QY 60 GIPARFSGSGGTDFTLNTHHPVEEDAATYYCOLCNEDEPTFGAGTKLELK 110
   |||||
Db 61 GVPARFSGSGGTDFTLNTHHPVEEDAATYYQHSRELPRTFGGGKLEIK 111
   |||||

RESULT 15
S45715
IG kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 07-May-1999
C:Accession: S45715
R:Kim, H.H.; Kato, K.; Yanato, S.; Igarashi, T.; Matsunaga, C.; Ohtsuka, H.; Higuchi, A.
FERS Lett. 346, 246-250, 1994
A:Title: Application of (13)C NMR spectroscopy to paratope mapping for larger antigen-Pa
A:Reference number: S45714; MUID:94283606; PMID:8013642
A:Accession: S45715
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-112 <KIM>
A:Experimental source: cell line Ex-3C7
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match      78.6%; Score 457.5; DB 2; Length 112;
Best Local Similarity 82.0%; Pred. No. 1.8e-34;
Matches 91; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSYVDYDGDSYM-WYQOKPGQPPKLLTYAASNLES 59
   |||||
Db 1 DIVLTQSPASLAVSLGORATISCRASKSVSTSGSYMHWYQOKPGQPPKLLIYLASNLES 60
   |||||

QY 60 GIPARFSGSGGTDFTLNTHHPVEEDAATYYCOLCNEDEPTFGAGTKLELK 110
   |||||
Db 61 GVPARFSGSGGTDFTLNTHHPVEEDAANYHCQHSRDLPLTFGAGTKLELK 111
   |||||

Search completed: January 14, 2004, 19:13:48
Job time : 15.7619 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 17:48:21 ; Search time 10 Seconds  
(without alignments)  
517.294 Million cell updates/sec

Title: US-09-759-112a-24

Perfect score: 582

Sequence: 1 DIVLTNSPASLAVSLGQRAT.....COLCNEDEPTFGAGTKLELK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533.5	91.7	111	1	KV3N_MOUSE
2	527.5	90.6	111	1	KV3M_MOUSE
3	523.5	89.9	111	1	KV3O_MOUSE
4	520.5	89.4	111	1	KV3Q_MOUSE
5	505	86.8	110	1	KV3P_MOUSE
6	503.5	86.5	111	1	KV3L_MOUSE
7	473.5	81.4	111	1	KV3S_MOUSE
8	470.5	80.8	111	1	KV3T_MOUSE
9	468.5	80.5	111	1	KV3R_MOUSE
10	455.5	78.3	111	1	KV3H_MOUSE
11	455.5	78.3	111	1	KV3K_MOUSE
12	454.5	78.1	111	1	KV3U_MOUSE
13	449.5	77.2	111	1	KV3J_MOUSE
14	448.5	77.1	131	1	KV3I_MOUSE
15	435.5	74.8	111	1	KV3C_MOUSE
16	433	74.4	112	1	KV3B_MOUSE
17	432.5	74.3	111	1	KV3A_MOUSE
18	430.5	74.0	108	1	KV3V_MOUSE
19	428.5	73.6	111	1	KV3D_MOUSE
20	424.5	72.9	112	1	KV3G_MOUSE
21	424.5	72.9	132	1	KV3F_MOUSE
22	392.5	67.4	111	1	KV3E_MOUSE
23	373.5	64.2	114	1	KV4C_HUMAN
24	371.5	63.8	134	1	KV4B_HUMAN
25	366	62.9	133	1	KV4S_HUMAN
26	352.5	60.6	108	1	KV5P_MOUSE
27	351	60.3	129	1	KV3H_HUMAN
28	350.5	60.2	108	1	KV1M_HUMAN
29	344	59.1	109	1	KV3D_HUMAN
30	343	58.9	129	1	KV3L_HUMAN
31	340	58.4	109	1	KV3F_HUMAN
32	339	58.2	109	1	KV3B_HUMAN
33	337.5	58.0	108	1	KV1K_HUMAN

34 337.5 58.0 129 1 KV1W\_HUMAN P04431 homo sapien  
35 336 57.7 129 1 KV3M\_HUMAN P18136 homo sapien  
36 335.5 57.6 108 1 KV1H\_HUMAN P01600 homo sapien  
37 333.5 57.3 108 1 KV1H\_HUMAN P01606 homo sapien  
38 333 57.2 113 1 KV2G\_MOUSE P01631 mus musculus  
39 331.5 57.0 108 1 KV1F\_HUMAN P01598 homo sapien  
40 331.5 57.0 108 1 KV1G\_HUMAN P01599 homo sapien  
41 329.5 56.6 121 1 KV4O\_HUMAN P06312 homo sapien  
42 328.5 56.4 108 1 KV1B\_HUMAN P01594 homo sapien  
43 328 56.4 133 1 KV1E\_HUMAN P06310 homo sapien  
44 327.5 56.3 108 1 KV1E\_HUMAN P01597 homo sapien  
45 327 56.2 109 1 KV3E\_HUMAN P01623 homo sapien

## ALIGNMENTS

RESULT 1  
KV3N\_MOUSE  
ID KV3N\_MOUSE STANDARD; PRT; 111 AA.  
AC P01666;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region PC 7183.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=79073152; PubMed=103003;  
RA Waigert M., Gammatan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
XT diversity.";  
RL Nature 276:785-790(1978).  
DR PIR; B01937; KVM83.  
DR HSP; P01679; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;  
  
Query Match 91.7%; Score 533.5; DB 1; Length 111;  
Best Local Similarity 94.6%; Pred. No. 1.8e-46;  
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
  
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSVYDGDGSM-WYQKPGQPPKLLTYAASNLES 59  
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSVYDGDGSMWYQKPGQPPKLLTYAASNLES 60  
QY 60 GIPARFSGSGGTDTFLNIHPVEEEDAATYTCOLCNEDEPTFGAGTKLELK 110  
Db 61 GIPARFSGSGGTDTFLNIHPVEEEDAATYTCQSNEDPLTFGAGTKLELK 111  
  
RESULT 2  
KV3M\_MOUSE  
ID KV3M\_MOUSE STANDARD; PRT; 111 AA.  
AC P01665;

21-JUL-1986 (Rel. 01, Created)  
21-JUL-1986 (Rel. 01, Last sequence update)  
15-JUL-1999 (Rel. 38, Last annotation update)  
Ig kappa chain V-III region PC 7043.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity.";  
RL Nature 276:785-790(1978).  
DR HSSP; P80362; IWL.  
DR InterPro; IPR007110; Ig-Like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;  
Query Match 90.8%; Score 527.5; DB 1; Length 111;  
Best Local Similarity 92.8%; Pred. No. 7.2e-46;  
Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYM-WYQOKPGOPPKLLTYAASNL 59  
DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSDYMNWYQOKPGOPPKLLTYAASNL 60  
QY 60 GIPARFSGSGGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEIK 110  
DB 61 GIPARFSGSGGDTFTLNHPVEEEDAATYCOQSNEDPTFGSGTKLEIK 111

RESULT 3  
KV3Q\_MOUSE STANDARD; PRT; 111 AA.  
AC P01667;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region PC 6308.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity.";  
RL Nature 276:785-790(1978).  
DR HSSP; P80362; IWL.  
DR InterPro; IPR007110; Ig-Like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;  
Query Match 89.9%; Score 523.5; DB 1; Length 111;  
Best Local Similarity 91.9%; Pred. No. 1.8e-45;  
Matches 102; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYM-WYQOKPGOPPKLLTYAASNL 59  
DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSDYMNWYQOKPGOPPKLLTYAASNL 60  
QY 60 GIPARFSGSGGDTFTLNHPVEEEDAATYCOLCNEDEPTFGAGTKLEIK 110  
DB 61 GIPARFSGSGGDTFTLNHPVEEEDAATYCOQSNEDPTFGSGTKLEIK 111

RESULT 4  
KV3Q\_MOUSE STANDARD; PRT; 111 AA.  
AC P01669;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region PC 7769.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity.";  
RL Nature 276:785-790(1978).  
DR HSSP; P80362; IWL.  
DR InterPro; IPR007110; Ig-Like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;  
Query Match 89.4%; Score 520.5; DB 1; Length 111;  
Best Local Similarity 91.0%; Pred. No. 3.6e-45;  
Matches 101; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYM-WYQOKPGOPPKLLTYAASNL 59  
DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSDYMNWYQOKPGOPPKLLTYAASNL 60

```

QY 60 GIPARFSGSGGDTFTLNHPVEEDAATYQCQCNEDPPTFGAGTKLEIK 110
DB 61 GIPARFSGSGGDTFTLNHPVEEDAATYQCQCNEDPPTFGAGTKLEIK 111

RESULT 5
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region FC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; D01937; KVM510.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 100
FT DOMAIN 101 110
FT DISULFID 23 92
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 86.8%; Score 505; DB 1; Length 110;
Best Local Similarity 90.1%; Pred. No. 1.2e-43;
Matches 100; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNL 59
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSLDYDGDSYM-WYQKPGQPPKLLTYAASNL 60

RESULT 6
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;

```

```

RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity; multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC !- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVM5C1.
DR HSP; P0362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 86.5%; Score 503.5; DB 1; Length 111;
Best Local Similarity 89.2%; Pred. No. 1.8e-43;
Matches 99; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNL 59
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLTYAASNL 60

QY 60 GIPARFSGSGGDTFTLNHPVEEDAATYQCQCNEDPPTFGAGTKLEIK 110
DB 61 GIPARFSGSGGDTFTLNHPVEEDAATYQCQCNEDPPTFGAGTKLEIK 111

RESULT 7
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region FC 7175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01938; KVM575.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

```

```

FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 81.4%; Score 473.5; DB 1; Length 111;
Best Local Similarity 85.8%; Pred. No. 1.7e-40;
Matches 95; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLITYAASNL 59
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVTSQSYMHYQKPGQPPKLLITYLASNL 60

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYYCOLCNEPPTFGAGTKLEK 110
Db 61 GVPARFSGSGGTDFTLNHPVEEDAAATYYCQHSRELPTFGAGTKLEK 111

RESULT 8
KV3T MOUSE
ID KV3T_MOUSE STANDARD; PRT; 111 AA.
AC P01670;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7940.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR HSP; P80362; IWT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12038 MW; E8A82306084352E CRC64;

Query Match 80.8%; Score 470.5; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 3.4e-40;
Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLITYAASNL 59
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVTSQSYMHYQKPGQPPKLLITYLASNL 60

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYYCOLCNEPPTFGAGTKLEK 110
Db 61 GVPARFSGSGGTDFTLNHPVEEDAAATYYCQHSRELPTFGAGTKLEK 111

RESULT 9
KV3R MOUSE
ID KV3R_MOUSE STANDARD; PRT; 111 AA.
AC P01670;

```

```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6684.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR HSP; P80362; IWT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 80.5%; Score 468.5; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 5.4e-40;
Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSYM-WYQKPGQPPKLLITYAASNL 59
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVTSQSYMHYQKPGQPPKLLITYLASNL 60

QY 60 GIPARFSGSGGTDFTLNHPVEEDAAATYYCOLCNEPPTFGAGTKLEK 110
Db 61 GVPARFSGSGGTDFTLNHPVEEDAAATYYCQHSRELPTFGAGTKLEK 111

RESULT 10
KV3H MOUSE
ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01650;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RT

```

```

RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
CC -1- MISCELLANEOUS: THE PC 3741 AND TPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A93204; KWS37.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 78.3%; Score 455.5; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 1.1e-38;
Matches 90; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSYDYDGSYM-WYQOKPGOPPKLLTYAASNL 59
DB 1 DIVLTQSPASLAVSLGORATISCRASESDVSNGSMFHWYQOKPGOPPKLLTYASNL 60
QY 60 GIPARFSGSGGDTFTLNHPVEEDAATYVYCOLCNEDEPPTFGAGTKLEIK 110
DB 61 GIPARFSGSGSRDTFTLNHPVEADVAITYVYCOQSNEDPTFGGATKLEIK 111

RESULT 11
KV3K MOUSE STANDARD; PRT; 111 AA.
ID KV3K MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
EL Nature 276:785-790 (1978).
CC -1- MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 78.3%; Score 455.5; DB 1; Length 111;
Best Local Similarity 82.9%; Pred. No. 1.3e-38;
Matches 92; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSYDYDGSYM-WYQOKPGOPPKLLTYAASNL 59
DB 1 DIVLTQSPASLAVSLGORATISCRASESDVSNGSMFHWYQOKPGOPPKLLTYASNL 60
QY 60 GIPARFSGSGGDTFTLNHPVEEDAATYVYCOLCNEDEPPTFGAGTKLEIK 110
DB 61 GIPARFSGSGSRDTFTLNHPVEADVAITYVYCOQSNEDPTFGGATKLEIK 111

RESULT 12
KV3U MOUSE STANDARD; PRT; 111 AA.
ID KV3U MOUSE STANDARD; PRT; 111 AA.
AC P01673;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 2485/PC 4039.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
EL Nature 276:785-790 (1978).
CC -1- MISCELLANEOUS: THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11986 MW; BF38CS9AA7858467 CRC64;

Query Match 78.1%; Score 454.5; DB 1; Length 111;
Best Local Similarity 82.0%; Pred. No. 1.1e-38;
Matches 91; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSYDYDGSYM-WYQOKPGOPPKLLTYAASNL 59
DB 1 DIVLTQSPASLAVSLGORATISCRASESDVSNGSMFHWYQOKPGOPPKLLTYASNL 60
QY 60 GIPARFSGSGGDTFTLNHPVEEDAATYVYCOLCNEDEPPTFGAGTKLEIK 110
DB 61 GIPARFSGSGSRDTFTLNHPVEADVAITYVYCOQSNEDPTFGAGTKLEIK 111

RESULT 13
KV3J MOUSE STANDARD; PRT; 111 AA.
ID KV3J MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```

DE Ig kappa chain V-III region ABPC 22/PC 9245.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE (ABPC 22).  
 RX MEDLINE=79012520; PubMed=99744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 related mouse kappa variable regions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).  
 RN [2]  
 RP SEQUENCE (PC 9245).  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 diversity.";  
 RL Nature 276:785-790 (1978).  
 CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.  
 DR HSP; P01679; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;  
 Query Match 77.2%; Score 449.5; DB 1; Length 111;  
 Best Local Similarity 80.2%; Pred. No. 4.2e-38;  
 Matches 89; Conservative 8; Mismatches 13; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNL 59  
 DB 1 NIVLTQSPASLAVSLGQRATISCRASESVDSYGNSEFWYQKPGQPPKLLTYLASNL 60  
 QY 60 GTPARFSGSGSTDTLTINHPVEEDAATYTCOLCNEPPTFGAGTKLELK 110  
 DB 61 GVPARFSGSGSTDTLTIDPVEADDAATYTCQNNEDPYTFGGTKLEIK 111  
 RESULT 14  
 KV3C MOUSE  
 ID KV3C MOUSE STANDARD; PRT; 131 AA.  
 AC P01651;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region MOPC 63 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-35.  
 RX MEDLINE=78235887; PubMed=98179;  
 RA Burstein Y., Schechter I.;  
 RT "Primary structures of N-terminal extra peptide segments linked to  
 the variable and constant regions of immunoglobulin light chain  
 precursors: implications on the organization and controlled  
 expression of immunoglobulin genes.";  
 RL Biochemistry 17:2392-2400 (1978).

RN [2]  
 RP SEQUENCE OF 21-131.  
 RX MEDLINE=73140225; PubMed=4691517;  
 RA McKean D.J., Potter M., Hood L.E.;  
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among  
 kappa chains with limited sequence differences.";  
 RL Biochemistry 12:760-771 (1973).  
 RN [3]  
 RP REVISIONS.  
 RX MEDLINE=79012520; PubMed=99744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 related mouse kappa variable regions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).  
 DR HSP; P01679; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.  
 FT DOMAIN 21 43  
 FT DOMAIN 44 58  
 FT DOMAIN 59 73  
 FT DOMAIN 74 80  
 FT DOMAIN 81 112  
 FT DOMAIN 113 121  
 FT DOMAIN 122 131  
 FT DISULFID 43 112  
 FT NON\_TER 131 131  
 SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;  
 Query Match 77.1%; Score 448.5; DB 1; Length 131;  
 Best Local Similarity 80.2%; Pred. No. 6.4e-38;  
 Matches 89; Conservative 8; Mismatches 13; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNL 59  
 DB 21 NIVLTQSPASLAVSLGQRATISCRASESVDSYGNSEFWYQKPGQPPKLLTYLASNL 80  
 QY 60 GTPARFSGSGSTDTLTINHPVEEDAATYTCOLCNEPPTFGAGTKLELK 110  
 DB 81 GVPARFSGSGSTDTLTIDPVEADDAATYTCQNNEDPYTFGGTKLEIK 131  
 RESULT 15  
 KV3C MOUSE  
 ID KV3C MOUSE STANDARD; PRT; 111 AA.  
 AC P01656;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region MOPC 70.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=67056897; PubMed=4162931;  
 RA Gray W.R., Dreyer W.J., Hood L.E.;  
 RT "Mechanism of antibody synthesis: size differences between mouse  
 kappa chains.";  
 RL Science 155:465-467 (1967).  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR HSP; P01679; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; ig; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PSS0835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON TER 111 111  
SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABG9DF0FC125 CRC64;  
  
Query Match 74.8%; Score 435.5; DB 1; Length 111;  
Best Local Similarity 76.8%; Pred. NO. 1e-36;  
Matches 85; Conservative 10; Mismatches 15; Indels 1; Gaps 1;  
  
Qy 1 DIVLTNSPASLAVSLGQRATISCKASQSVYDGDSYM-WYQKPGQPPKLLTYAASNLES 59  
Db 1 DIVLTQSPASLAVSLGQRATISCRASESVDNSGISPMNWFQKPGQPPKLLIYAASNQGS 60  
  
Qy 60 GIPARFSGSGCTDFTLNHPVEERDAATYQCLCNEDPPTGAGTKLEK 110  
Db 61 GVPARFSGSGGTDFTSLNHPHEEDDTAMVFCQQSKEVPTFGGTKLEIK 111

Search completed: January 14, 2004, 19:11:51  
Job time : 10 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 18:55:07 ; Search time 33.3333 Seconds  
(without alignments)  
851.574 Million cell updates/sec

Title: US-09-759-112A-24  
Perfect score: 582  
Sequence: 1 DIVLNSPASLAVSLGQRAT.....COLCNEDEPTFGAGTKLELK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTEMBL.23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467.5	80.3	111	11 Q920E9	Q920E9 mus musculus
2	413.5	71.0	103	11 Q9JL80	Q9JL80 mus musculus
3	352.5	60.6	108	4 Q9UL70	Q9UL70 homo sapien
4	348.5	59.9	108	4 Q9UL79	Q9UL79 homo sapien
5	346	59.9	109	4 Q9UL78	Q9UL78 homo sapien
6	342	58.8	238	11 Q9VCI6	Q9VCI6 mus musculus
7	341.5	58.7	108	4 Q9UL77	Q9UL77 homo sapien
8	341.5	58.7	234	4 Q9NEK1	Q9NEK1 homo sapien
9	341	58.6	107	4 Q9GSA9	Q9GSA9 homo sapien
10	340	58.4	112	11 Q8K1F2	Q8K1F2 mus musculus
11	338.5	58.2	108	4 Q9UL83	Q9UL83 homo sapien
12	335	57.6	109	4 Q9UL85	Q9UL85 homo sapien
13	335	57.6	112	11 Q8K1F3	Q8K1F3 mus musculus
14	334	57.4	238	11 Q99M37	Q99M37 mus musculus
15	334	57.4	239	4 Q8TCD0	Q8TCD0 homo sapien
16	330	56.7	114	11 Q8K1F1	Q8K1F1 mus musculus

17	327	56.2	239	11 Q8VC55	Q8VC55 mus musculus
18	325.5	55.9	114	4 Q9UL80	Q9UL80 homo sapien
19	325	55.8	107	4 Q9UL81	Q9UL81 homo sapien
20	324	55.7	239	4 Q8NEK0	Q8NEK0 homo sapien
21	321.5	55.2	108	11 Q8VIJ0	Q8VIJ0 mus musculus
22	314	54.0	106	5 Q9U410	Q9U410 schistosoma
23	313.5	53.9	214	11 Q9RIAS	Q9RIAS mus musculus
24	312	53.6	239	11 Q8KOF8	Q8KOF8 mus musculus
25	311	53.4	109	4 Q9UL86	Q9UL86 homo sapien
26	311	53.4	112	11 Q8K1F0	Q8K1F0 mus musculus
27	309.5	53.2	107	11 Q9RZ9	Q9RZ9 mus musculus
28	308	52.9	134	11 Q8VDD0	Q8VDD0 mus musculus
29	306.5	52.7	234	11 Q9LWF8	Q9LWF8 mus musculus
30	305.5	52.5	234	11 Q8R062	Q8R062 mus musculus
31	305	52.4	104	11 Q9JL82	Q9JL82 mus musculus
32	305	52.4	235	11 Q9LW12	Q9LW12 mus musculus
33	304.5	52.3	218	11 Q925S1	Q925S1 mus musculus
34	301.5	51.8	99	11 Q9JL74	Q9JL74 mus musculus
35	299.5	51.5	233	11 Q9LWS9	Q9LWS9 mus musculus
36	294.5	50.6	234	11 Q8VCP0	Q8VCP0 mus musculus
37	293.5	50.4	298	11 Q9QYF0	Q9QYF0 mus musculus
38	291.5	50.1	109	11 Q920E6	Q920E6 mus musculus
39	289.5	49.7	107	11 Q9JL84	Q9JL84 mus musculus
40	288.5	49.6	116	4 Q96PF6	Q96PF6 homo sapien
41	288.5	49.6	234	11 Q8R028	Q8R028 mus musculus
42	286.5	49.2	57	11 Q9UL76	Q9JL76 mus musculus
43	283.5	48.7	101	11 Q9UL78	Q9JL78 mus musculus
44	280	48.1	148	11 Q8K122	Q8K122 mus musculus
45	279.5	48.0	109	6 Q9N0W5	Q9N0W5 oryctolagus

## ALIGNMENTS

RESULT 1  
Q920E9 PRELIMINARY; PRT; 111 AA.  
AC Q920E9: 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Pterin-mimicking anti-idiotope kappa chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed  
in Mammalian Cells."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307935; AAL09419.1; -.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
FT NON\_TER 1 111  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12046 MW; 1E46989AA6858526 CRC64;

Query Match 80.3%; Score 467.5; DB 11; Length 111;  
Best Local Similarity 83.8%; Pred No. 1.5e-43;  
Matches 93; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

Qy 1 DIVLNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQQPQPPLTYAASNTLES 59  
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQQPQPPLTYAASNTLES 60  
Qy 60 GIPARFSGSGSTDFTLNHPVEEEDATYYCOLCNEDEPTFGAGTKLELK 110

Db 61 GVPARFSGSGSDTFLNHPVEEDATYYCQSRRLPYTFGGGKLEIK 111  
 RESULT 2  
 Q9JL80  
 ID Q9JL80 PRELIMINARY; PRT; 103 AA.  
 AC Q9JL80  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Anti-myosin immunoglobulin light chain variable region  
 (fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RC MEDLINE=20448942; PubMed=10992488;  
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
 RA "T-Cell-dependent antibody response to the dominant epitope of  
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reac-  
 RT with cardiac myosin.";  
 RL Infect. Immun. 68:5803-5808 (2000).  
 DR ENBL; AF205026; BAF69324.1; -.  
 DR HSP; P80382; IWLW.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 103  
 FT NON\_TER 103  
 SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;  
 Query Match 71.0%; Score 413.5; DB 11; Length 103;  
 Best Local Similarity 77.7%; Pred. No. 1.1e-37;  
 Matches 80; Conservative 10; Mismatches 12; Indels 1;  
 QY 9 ASLAVSLGGRATISCKASQSDYDGDYSW-VYQKPGQPPKLLTYAASNLESGIPV  
 Db 1 ASLAVSLGGRATISCRASESVYIGTSLMQYQKPGQPPKLLIYAASNVESGVPV  
 QY 68 SSGSGTDFTLNHPVEEDATYYCOLCNEDPFTFGAGTKLEIK 110  
 Db 61 SSGSGTDFSLNHPVEEDDIAMFYCQSRKVPWTFTGGGKLEIK 103  
 RESULT 3  
 Q9JL70  
 ID Q9JL70 PRELIMINARY; PRT; 108 AA.  
 AC Q9JL70  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR ENBL; AF035044; AAD56280.1; -

Q9UL78;  
 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035036; AAD56272.1; -;  
 DR HSP; P80362; IWT.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 109  
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;  
 Query Match 59.5%; Score 346; DB 4; Length 109;  
 Best Local Similarity 62.2%; Pred. No. 3e-30;  
 Matches 69; Conservative 14; Mismatches 24; Indels 4; Gaps 2;  
 QY 1 DIVLTNSPASLAVSLGORATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLE 59  
 Db EIVLTQSPGTLSPGSRATLSCRASQSV---SSSYLAWYQKPGQAPRLIYGASSRAT 57  
 QY 60 GIPARFSGSGGTDFTLNIHPVEEEDAAATYCOLCNEDEPTFGAGTKLELK 110  
 Db GIPDRFSGSGGTDFTLTISRLEPEDCAVYQQYGGSSPLTFGGTKVRIK 108  
 RESULT 6  
 Q8VC16 PRELIMINARY; PRT; 238 AA.  
 ID Q8VC16  
 AC Q8VC16;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE Hypothetical 26.2 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019760; AAH19760.1; -;  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;  
 Query Match 58.8%; Score 342; DB 11; Length 238;  
 Best Local Similarity 60.7%; Pred. No. 2.2e-29;  
 Matches 68; Conservative 14; Mismatches 28; Indels 2; Gaps 2;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLE 58  
 Db DVVMTQIFLSLPVSLGDDQASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 79  
 QY 59 SCIPARFSGSGGTDFTLNIHPVEEEDAAATYCOLCNEDEPTFGAGTKLELK 110  
 Db SGVPDRFSGSGGTDFTLKISRVEAEDLGVVFCQSQTHTVPTFGGTYKLEIK 131  
 RESULT 7  
 Q9UL77 PRELIMINARY; PRT; 108 AA.  
 ID Q9UL77  
 AC Q9UL77;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035037; AAD56273.1; -;  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;  
 Query Match 58.7%; Score 341.5; DB 4; Length 108;  
 Best Local Similarity 60.4%; Pred. No. 9.2e-30;  
 Matches 67; Conservative 17; Mismatches 22; Indels 5; Gaps 2;  
 QY 1 DIVLTNSPASLAVSLGORATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLE 59  
 Db DIQWTQSPSSLASVGDRTVITCRASQSI---SSYLWYQKPGKAPNLLIYAASLQS 56  
 QY 60 GIPARFSGSGGTDFTLNIHPVEEEDAAATYCOLCNEDEPTFGAGTKLELK 110  
 Db GVPSRFSGSGGTDFTLTITSLQPEDFATYQQSYSTSTWTGEGTKVRIK 107  
 RESULT 8  
 Q8NEK1 PRELIMINARY; PRT; 234 AA.  
 ID Q8NEK1  
 AC Q8NEK1;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC030813; AAH30813.1; -;

AC	Q9K1F2;
AD	01-OCT-2002 (TrEMBLrel. 22, Created)
AE	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
AF	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
AG	Anti-Vipase light chain variable region (Fragment).
AH	Mus musculus (Mouse)
AI	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AJ	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AK	NCBI_TaxID=10090;
AL	[1]
AM	SEQUENCE FROM N.A.
AN	STRAIN=BALB/C; TISSUE=Hyperimmunized spleen;
AO	Zhou Y.-X., Taguchi H., Elaque S., Karle S., Nishiyama Y., Paul S.;
AP	"Innate proteolytic antibodies: Failed D-Vipase response to the D-
AQ	RT anticloner of VIP and identification of L-Vipase VL domains.";
AR	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
AS	EMBL; AF516283; AAM64201.1; -
AT	InterPro; IPR003599; IG.
AV	InterPro; IPR007110; IG-like.
AW	InterPro; IPR003006; IG_MHC.
AX	InterPro; IPR003596; IG_V.
AY	Pfam; PF00047; IG; 1.
AZ	SMART; SM00409; IGV; 1.
B0	SMART; SM00406; IGV; 1.
B1	PROSITE; PS50835; IG LIKE; 1.
B2	NON_TER 1 112 112
B3	FT NON_TER 1 112 112
B4	SEQUENCE 112 AA; 11953 MW; 4716887FADB543ED CRC64;
B5	Query Match 58.4%; Score 340; DB 11; Length 112;
B6	Best Local Similarity 63.1%; Pred. No. 1.4e-29;
B7	Matches 70; Conservative 12; Mismatches 23; Indels 6; Gaps 2;
B8	
B9	
C0	
C1	
C2	
C3	
C4	
C5	
C6	
C7	
C8	
C9	
D0	
D1	
D2	
D3	
D4	
D5	
D6	
D7	
D8	
D9	
E0	
E1	
E2	
E3	
E4	
E5	
E6	
E7	
E8	
E9	
F0	
F1	
F2	
F3	
F4	
F5	
F6	
F7	
F8	
F9	
G0	
G1	
G2	
G3	
G4	
G5	
G6	
G7	
G8	
G9	
H0	
H1	
H2	
H3	
H4	
H5	
H6	
H7	
H8	
H9	
I0	
I1	
I2	
I3	
I4	
I5	
I6	
I7	
I8	
I9	
J0	
J1	
J2	
J3	
J4	
J5	
J6	
J7	
J8	
J9	
K0	
K1	
K2	
K3	
K4	
K5	
K6	
K7	
K8	
K9	
L0	
L1	
L2	
L3	
L4	
L5	
L6	
L7	
L8	
L9	
M0	
M1	
M2	
M3	
M4	
M5	
M6	
M7	
M8	
M9	
N0	
N1	
N2	
N3	
N4	
N5	
N6	
N7	
N8	
N9	
O0	
O1	
O2	
O3	
O4	
O5	
O6	
O7	
O8	
O9	
P0	
P1	
P2	
P3	
P4	
P5	
P6	
P7	
P8	
P9	
Q0	
Q1	
Q2	
Q3	
Q4	
Q5	
Q6	
Q7	
Q8	
Q9	
R0	
R1	
R2	
R3	
R4	
R5	
R6	
R7	
R8	
R9	
S0	
S1	
S2	
S3	
S4	
S5	
S6	
S7	
S8	
S9	
T0	
T1	
T2	
T3	
T4	
T5	
T6	
T7	
T8	
T9	
U0	
U1	
U2	
U3	
U4	
U5	
U6	
U7	
U8	
U9	
V0	
V1	
V2	
V3	
V4	
V5	
V6	
V7	
V8	
V9	
W0	
W1	



Search completed: January 14, 2004, 19:13:15  
Job time : 36.3333 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 19:10:12 ; Search time 13.8095 Seconds  
(without alignments)  
337.028 Million cell updates/sec

Title: US-09-759-112a-24  
Perfect score: 582  
Sequence: 1 DIVLTNSPASLAVSLQCRAT.....COLCNEBPPTFGAGTKLELK 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/2/iaa/5A COMB pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B COMB pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A COMB pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B COMB pep.\*  
5: /cgn2\_6/prodata/2/iaa/6C COMB pep.\*  
6: /cgn2\_6/prodata/2/iaa/6D COMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	537.5	92.4	132	2	US-08-483-636-2
2	537.5	92.4	132	2	US-08-483-632-2
3	519.5	89.3	111	1	US-08-491-845-8
4	516.5	88.7	131	3	US-08-579-378A-14
5	503.5	86.5	106	3	US-08-466-151-6
6	503.5	86.5	106	4	US-08-466-151-6
7	491.5	84.5	111	3	US-08-466-151-2
8	491.5	84.5	111	4	US-08-466-151-2
9	490.5	84.3	120	1	US-08-111-080-24
10	490.5	84.3	120	1	US-08-211-980-24
11	490.5	84.3	120	5	PCT-US93-07967-24
12	485.5	83.4	111	3	US-08-887-352B-5
13	485.5	83.4	111	3	US-09-109-207C-5
14	485.5	83.4	111	3	US-09-296-005-5
15	469.5	80.7	131	2	US-08-483-636-58
16	469.5	80.7	131	2	US-08-483-632-58
17	465.5	80.0	131	1	US-08-137-117D-33
18	465.5	80.0	131	2	US-08-436-717-33
19	463.5	79.6	131	2	US-08-483-636-14
20	463.5	79.6	131	2	US-08-483-632-14
21	460.5	79.1	131	1	US-08-137-117D-25
22	460.5	79.1	131	2	US-08-436-717-25
23	456.5	78.4	131	2	US-08-621-751A-10
24	453.5	77.9	111	1	US-08-275-053-11
25	453.5	77.9	121	1	US-08-111-080-22
26	453.5	77.9	121	1	US-08-211-980-22
27	453.5	77.9	121	5	PCT-US93-07967-22

28	449.5	77.2	111	2	US-08-483-636-73	Sequence 73, Appl
29	449.5	77.2	111	2	US-08-483-632-73	Sequence 73, Appl
30	448.5	77.1	129	4	US-09-556-605-2	Sequence 2, Appl
31	447	76.8	151	4	US-09-318-786-33	Sequence 33, Appl
32	446.5	76.7	120	1	US-08-111-080-26	Sequence 26, Appl
33	446.5	76.7	120	1	US-08-211-980-26	Sequence 26, Appl
34	446.5	76.7	120	5	PCT-US93-07967-26	Sequence 26, Appl
35	444.5	76.4	111	1	US-08-207-169A-4	Sequence 4, Appl
36	444.5	76.4	121	1	US-08-111-080-18	Sequence 18, Appl
37	444.5	76.4	121	1	US-08-211-980-18	Sequence 18, Appl
38	444.5	76.4	121	5	PCT-US93-07111-17	Sequence 17, Appl
39	444.5	76.4	121	5	PCT-US93-07967-18	Sequence 18, Appl
40	444	76.3	110	1	US-08-017-570-2	Sequence 2, Appl
41	444	76.3	110	1	US-08-471-426-2	Sequence 2, Appl
42	444	76.3	110	4	US-09-672-609-13	Sequence 13, Appl
43	444	76.3	110	4	US-09-025-403A-13	Sequence 13, Appl
44	444	76.3	110	5	PCT-US94-01709-2	Sequence 2, Appl
45	439.5	75.5	132	2	US-08-379-057-16	Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-08-483-636-2  
; Sequence 2, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-483-636-2

Query Match 92.4%; Score 537.5; DB 2; Length 132;  
Best Local Similarity 93.7%; Pred. No. 2.2e-49;  
Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;  
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLES 59  
DB 21 DIVLTQSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLES 80  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLCNEDEPTFGAGTKLEK 110  
DB 81 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQNSNEDPTFGGKTLEIK 131

## RESULT 2

US-08-483-632-2  
; Sequence 2, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
ATTORNEY/AGENT INFORMATION:  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-632-2

Query Match 92.4%; Score 537.5; DB 2; Length 132;  
Best Local Similarity 93.7%; Pred. No. 2.2e-49;  
Matches 104; Conservative 1; Mismatches 5; Indels 1; Gaps 1;  
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLES 59

DB 21 DIVLTQSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLES 80  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLCNEDEPTFGAGTKLEK 110  
DB 81 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQNSNEDPTFGGKTLEIK 131

## RESULT 3

US-08-491-845-8  
; Sequence 8, Application US/08491845  
; Patent No. 5773247  
; GENERAL INFORMATION:  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: EDA, Yasuyuki  
; APPLICANT: SHIOSAKI, Kouichi  
; APPLICANT: OSATOMI, Kiyoshi  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND  
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/491,845  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00039  
FILING DATE: 14-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: MAEDA=5  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-491-845-8

Query Match 89.3%; Score 519.5; DB 1; Length 111;  
Best Local Similarity 91.9%; Pred. No. 1.4e-47;  
Matches 102; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 DIVLTNSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLES 59  
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSYVDYDGSYM-WYQKPGQPPKLLTYAASNLES 60  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLCNEDEPTFGAGTKLEK 110  
DB 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQNSNEDPTFGGKTLEIK 111

## RESULT 4

US-08-579-378A-14  
; Sequence 14, Application US/08579378A  
; Patent No. 6210671  
; GENERAL INFORMATION:



APPLICANT: Co, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
TITLE OF INVENTION: L-Selectin  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/579,378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,074  
FILING DATE: 30-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschultz, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-579-378A-14

Query Match 88.7%; Score 516.5; DB 3; Length 131;  
Best Local Similarity 90.1%; Pred. No. 3.5e-47;  
Matches 100; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDYSY-WYQKQGPQPKLLTYAASNLES 59  
Db 21 DIVLTQSPASLSVLSGERASISCKASQSDYDGDYSYMWYQKQGPQPKLLTYAASNLES 80

QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQLCNEDPPTFGAGTKLEK 110  
Db 81 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQNSNEDPPTFGGTTKLEIK 131

RESULT 5  
US-08-466-151-6  
Sequence 6, Application US/08466151  
Patent No. 6037453  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,151  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/466163  
FILING DATE: 06-Jun-1995  
APPLICATION NUMBER: 08/405617  
FILING DATE: 15-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/185899  
FILING DATE: 26-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/879495  
FILING DATE: 07-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P2C1D1  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-466-151-6

Query Match 86.5%; Score 503.5; DB 3; Length 106;  
Best Local Similarity 93.4%; Pred. No. 6.4e-46;  
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDYSY-WYQKQGPQPKLLTYAASNLES 59  
Db 1 DIQLTQSPASLAVSLGQRATISCKASQSDYDGDYSYMWYQKQGPQPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQLCNEDPPTFGAGT 105  
Db 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQNSNEDPPTFGAGT 106

RESULT 6  
US-08-466-163B-6  
Sequence 6, Application US/08466163B  
Patent No. 6328509  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
CURRENT FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64

```

; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-6

Query Match      86.5%; Score 503.5; DB 4; Length 106;
Best Local Similarity 93.4%; Pred. No. 6.4e-46;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSTM-WYQKPGPPKLLTYAASNLES 59
Db 1 DIQLTSPASLAVSLGORATISCKASQSDYDGDSTMWYQKPGPPKLLTYAASNLES 60

Qy 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLCNEDEPTFGAGTKLEIK 105
Db 61 GIPARFSGSGGTDFTLNHPVEEEDAATYYCQNSNEDEPTFGAGTK 106

RESULT 7
US-08-466-151-2
; Sequence 2, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Syvoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P07182C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-2

Query Match      84.5%; Score 491.5; DB 3; Length 111;

```

```

Best Local Similarity 88.3%; Pred. No. 1.2e-44;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSTM-WYQKPGPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSTMWYQKPGPPILLIYAASVILGS 60

Qy 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLCNEDEPTFGAGTKLEIK 110
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAATFYCQSHEDPTTFGAGTKLEIK 111

RESULT 8
US-08-466-163B-2
; Sequence 2, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P07182C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-2

Query Match      84.5%; Score 491.5; DB 4; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.2e-44;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSTM-WYQKPGPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSTMWYQKPGPPILLIYAASVILGS 60

Qy 60 GIPARFSGSGGTDFTLNHPVEEEDAATYYCOLCNEDEPTFGAGTKLEIK 110
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAATFYCQSHEDPTTFGAGTKLEIK 111

RESULT 9
US-08-111-080-24
; Sequence 24, Application 08/111080
; Patent No. 5558865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: 08/111,080  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/748,562  
 FILING DATE: 22-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/07111  
 FILING DATE: 24-AUG-1992  
 APPLICATION DATA:  
 APPLICATION NUMBER: US 08/039,457  
 FILING DATE: 22-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Borun, Michael F.  
 REGISTRATION NUMBER: 25,447  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 120 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-111-080-24

Query Match 84.3%; Score 490.5; DB 1; Length 120;  
 Best Local Similarity 87.3%; Pred. No. 1.7e-44;  
 Matches 96; Conservative 3; Mismatches 10; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYK-WYQKPGOPPKLLTYAASNL 59  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSDYK-WYQKPGOPPKLLTYAASNL 60  
 QY 60 GIPARFSGSGGDTFTLNHPVEEEDATYYQQLCNEEDPTFGAGTKLEL 109  
 Db 61 GIPARFYGSGGDTFTNTIHPVEEEDATYYQQLCNEEDPTFGAGTKLEI 110

RESULT 10  
 US-08-211-980-24  
 Sequence 24, Application US/08211980  
 Patent No. 5665569  
 GENERAL INFORMATION:  
 APPLICANT: Ohno, Tsuneya  
 TITLE OF INVENTION: HIV Immunotherapeutics  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ADDRESS: Borun  
 STREET: 6300 Sears Tower, 233 S. Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/211,980  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/07111  
 FILING DATE: 24-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/039,457  
 FILING DATE: 22-APR-1993  
 ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.  
 REGISTRATION NUMBER: 25,447  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 120 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-211-980-24  
 Query Match 84.3%; Score 490.5; DB 1; Length 120;  
 Best Local Similarity 87.3%; Pred. No. 1.7e-44;  
 Matches 96; Conservative 3; Mismatches 10; Indels 1; Gaps 1;  
 QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDSDYK-WYQKPGOPPKLLTYAASNL 59  
 Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSDYK-WYQKPGOPPKLLTYAASNL 60  
 QY 60 GIPARFSGSGGDTFTLNHPVEEEDATYYQQLCNEEDPTFGAGTKLEL 109  
 Db 61 GIPARFYGSGGDTFTNTIHPVEEEDATYYQQLCNEEDPTFGAGTKLEI 110

RESULT 11  
 PCT-US93-07967-24  
 Sequence 24, Application PC/TUS9307967  
 GENERAL INFORMATION:  
 APPLICANT: Ohno, Tsuneya  
 TITLE OF INVENTION: HIV Immunotherapeutics  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ADDRESS: Borun  
 STREET: 6300 Sears Tower, 233 S. Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/07967  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/07111  
 FILING DATE: 24-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/039,457  
 FILING DATE: 22-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Borun, Michael F.  
 REGISTRATION NUMBER: 25,447  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 120 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US93-07967-24

```
Query Match      84.3%; Score 490.5; DB 5; Length 120;
Best Local Similarity 87.3%; Pred. No. 1.7e-44;
Matches 96; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDYSYMWYQKPGQPPKLLTYAASNLES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSHEDPPTFGAGTKLEIK 110
Db 61 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSHEDPPTFGAGTKLEIK 110

RESULT 12
US-08-887-352B-5
; Sequence 5, Application US/08897352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svcboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-5

Query Match      83.4%; Score 485.5; DB 2; Length 111;
Best Local Similarity 87.4%; Pred. No. 5.3e-44;
Matches 97; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIQLTQSPASLAVSLGORATISCKASQSDYDGDYSYMWYQKPGQPPKLLTYAASYLGS 60
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSHEDPPTFGAGTKLEIK 110
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSHEDPPTFGAGTKLEIK 111

RESULT 13
US-09-109-207C-5
; Sequence 5, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
```

```
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 5
LENGTH: 111
TYPE: PRT
ORGANISM: Mus musculus
US-09-109-207C-5

Query Match      83.4%; Score 485.5; DB 3; Length 111;
Best Local Similarity 87.4%; Pred. No. 5.3e-44;
Matches 97; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIQLTQSPASLAVSLGORATISCKASQSDYDGDYSYMWYQKPGQPPKLLTYAASYLGS 60
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSHEDPPTFGAGTKLEIK 110
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSHEDPPTFGAGTKLEIK 111

RESULT 14
US-09-296-005-5
; Sequence 5, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide:
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-296-005-5

Query Match      83.4%; Score 485.5; DB 3; Length 111;
Best Local Similarity 87.4%; Pred. No. 5.3e-44;
Matches 97; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIQLTQSPASLAVSLGORATISCKASQSDYDGDYSYMWYQKPGQPPKLLTYAASYLGS 60
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSHEDPPTFGAGTKLEIK 110
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAAATYQCQSHEDPPTFGAGTKLEIK 111

RESULT 15
US-08-483-636-58
; Sequence 58, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
```

STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,636  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5030  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-636-58

Query Match 80.7%; Score 469.5; DB 2; Length 131;  
Best Local Similarity 80.2%; Pred. No. 3.1e-42;  
Matches 89; Conservative 8; Mismatches 13; Indels 1; Gaps 1;  
QY 1 DIVLTNSPASLAVSLGRATISKASQSYDYGDSYM-WYQOKPGQPPKLLIYAASNLES 59  
Db 20 DIVMTQSPDLSLAVSLGRATINCKASQSYDYGDSYMNWYQOKPGQPPKLLIYAASNLES 79  
QY 60 GIPARFSGSGGTDFTLNHPVEEDATYYCQLCNEDPPTFGAGTKLELK 110  
Db 80 GVPDRFSGSGGTDFTLTITSSQLAEDVAVYYCQSNEDPPTFGGKVEIK 130

Search completed: January 14, 2004, 19:14:24  
Job time : 14.8095 secs





```

; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-4

Query Match
Best Local Similarity 90.5%; Score 526.5; DB 10; Length 238;
Matches 103; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
Db 21 DIVLTQSPASLAVSLGORATISCKASQSDYDGDYSYNNWYQKPGQPPKLLTYAASNLES 80
QY 60 GIPARFSGSGGTDFTLNHPVEEDAATYYCOLCNEDEPPTFGAGTKLEK 110
Db 81 GIPARFSGSGGTDFTLNHPVEEDAATYYCOQTNEDEFTWGGTKLEIK 131

RESULT 6
US-10-194-975-115
; Sequence 115, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 115
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-194-975-115

Query Match
Best Local Similarity 86.9%; Score 505.5; DB 15; Length 112;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIVLTQSPVSLAVSGVQRTATISCKASQSDYDGDYSYNNWYQKPGQPPKLLTYVVSNLES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEDAATYYCOLCNEDEPPTFGAGTKLEK 110
Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPLTFGAGTNLEK 111

RESULT 7
US-09-802-077-6
; Sequence 6, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Paula M.
; APPLICANT: Jardieu, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617

```

```

; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-6

Query Match
Best Local Similarity 86.5%; Score 503.5; DB 9; Length 106;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIQLTQSPASLAVSLGORATISCKASQSDYDGDYSYNNWYQKPGQPPKLLTYAASNLES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEDAATYYCOLCNEDEPPTFGAGT 105
Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPPTFGAGT 106

RESULT 8
US-09-802-096-6
; Sequence 6, Application US/09802096
; Patent No. US2001003839A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3U9
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-6

Query Match
Best Local Similarity 86.5%; Score 503.5; DB 9; Length 106;
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGORATISCKASQSDYDGDYSY-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIQLTQSPASLAVSLGORATISCKASQSDYDGDYSYNNWYQKPGQPPKLLTYAASNLES 60
QY 60 GIPARFSGSGGTDFTLNHPVEEDAATYYCOLCNEDEPPTFGAGT 105
Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYYCQSNEDPPTFGAGT 106

RESULT 9
US-09-925-179-6
; Sequence 6, Application US/09925179

```



Publication No. US20030044858A1  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Anti-IGE Antibodies (as amended)  
FILE REFERENCE: P0718P2C1D1C1US  
CURRENT APPLICATION NUMBER: US/09/925,179  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 08/466,163  
PRIOR FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: PCT/US92/06860  
PRIOR FILING DATE: 1992-08-14  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 68  
SEQ ID NO 6  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-925-179-6

Query Match 86.5%; Score 503.5; DB 11; Length 106;  
Best Local Similarity 93.4%; Pred. No. 9.9e-42;  
Matches 99; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSDYM-WYQKPGPPKLLTYAASNLES 59  
Db 1 DIQLTQSPASLAVSLGQRATISCKASQSDYDGDSDYM-WYQKPGPPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 105  
Db 61 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 106

RESULT 10  
US-09-802-077-2  
Sequence 2, Application US/09802077  
Patent No. US20010033842A1  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
FILE REFERENCE: P0718P2C2US  
CURRENT APPLICATION NUMBER: US/09/802,077  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: PCT/US92/06860  
PRIOR FILING DATE: 1992-08-14  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64  
SEQ ID NO 2  
LENGTH: 111  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-802-077-2

Query Match 84.5%; Score 491.5; DB 9; Length 111;  
Best Local Similarity 88.3%; Pred. No. 1.5e-40;  
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSDYM-WYQKPGPPKLLTYAASNLES 59  
Db 1 DIQLTQSPASLAVSLGQRATISCKASQSDYDGDSDYM-WYQKPGPPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 110  
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 111

RESULT 12  
US-09-925-179-2  
Sequence 2, Application US/09925179  
Publication No. US20030044858A1  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Anti-IGE Antibodies (as amended)  
FILE REFERENCE: P0718P2C1D1C1US  
CURRENT APPLICATION NUMBER: US/09/925,179  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 08/466,163  
PRIOR FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: PCT/US92/06860  
PRIOR FILING DATE: 1992-08-14  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 68

Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYM-WYQKPGPPKLLTYAASNLES 60  
QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 110  
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 111

RESULT 11  
US-09-802-096-2  
Sequence 2, Application US/09802096  
Patent No. US20010038839A1  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
FILE REFERENCE: P0718P2C3US  
CURRENT APPLICATION NUMBER: US/09/802,096  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: PCT/US92/06860  
PRIOR FILING DATE: 1992-08-14  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64  
SEQ ID NO 2  
LENGTH: 111  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-802-096-2

Query Match 84.5%; Score 491.5; DB 9; Length 111;  
Best Local Similarity 88.3%; Pred. No. 1.5e-40;  
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 DIVLTNSPASLAVSLGQRATISCKASQSDYDGDSDYM-WYQKPGPPKLLTYAASNLES 59  
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYM-WYQKPGPPKLLTYAASNLES 60

QY 60 GIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 110  
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAAATYCOLCNEDEPPTFGAGT 111

RESULT 12  
US-09-925-179-2  
Sequence 2, Application US/09925179  
Publication No. US20030044858A1  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Anti-IGE Antibodies (as amended)  
FILE REFERENCE: P0718P2C1D1C1US  
CURRENT APPLICATION NUMBER: US/09/925,179  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 08/466,163  
PRIOR FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: PCT/US92/06860  
PRIOR FILING DATE: 1992-08-14  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 68

```
; SEQ ID NO 2
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-179-2

Query Match      84.5%; Score 491.5; DB 11; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.5e-40;
Matches 98; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIVLTQSPGTLSPGERATLSCKASQSDVDGDSYNNWYQKPGQPPKLLTYAASNLES 60
Qy 60 GIPARFSGSGGTDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEIK 110
Db 61 EIPARFSGSGGTDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEIK 111

RESULT 13
US-10-160-506-81
; Sequence 81, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
; FILE REFERENCE: 1048-182001
; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-160-506-81

Query Match      84.2%; Score 490; DB 12; Length 112;
Best Local Similarity 85.7%; Pred. No. 2.2e-40;
Matches 96; Conservative 7; Mismatches 7; Indels 2; Gaps 2;

Qy 1 DIVLTNSPASLAVSLGORATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 1 DIVLTQSPGTLSPGERATISCKASQSDVDGDSYNNWYQKPGQPPKLLTYAASNLES 60
Qy 60 GIPARFSGSGGTDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEIK 110
Db 61 GVPARFSGSGGTDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEIK 112

RESULT 14
US-10-384-933-54
; Sequence 54, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
```

```
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 54
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed light
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-54

Query Match      83.8%; Score 487.5; DB 12; Length 238;
Best Local Similarity 83.8%; Pred. No. 8.8e-40;
Matches 93; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 21 DIVLTQSPGTLSPGERATLSCKASQSDVDGDSYNNWYQKPGQPPKLLTYAASNLES 80
Qy 60 GIPARFSGSGGTDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEIK 110
Db 81 GIPDRFSGSGGTDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEIK 131

RESULT 15
US-10-216-484-54
; Sequence 54, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 54
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed light
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-54

Query Match      83.8%; Score 487.5; DB 15; Length 238;
Best Local Similarity 83.8%; Pred. No. 8.8e-40;
Matches 93; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

Qy 1 DIVLTNSPASLAVSLGORATISCKASQSDVDGDSYM-WYQKPGQPPKLLTYAASNLES 59
Db 21 DIVLTQSPGTLSPGERATLSCKASQSDVDGDSYNNWYQKPGQPPKLLTYAASNLES 80
Qy 60 GIPARFSGSGGTDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEIK 110
Db 81 GIPDRFSGSGGTDFTLNHPVEEEDAATYQCQSNEDPPTFGAGTKLEIK 131

Search completed: January 14, 2004, 19:25:04
Job time : 153.81 secs
```